



XX 17-MAR-1995; 95MO-US003426.  
 XX 18-MAR-1994; 94US-00215139.  
 PR 05-AUG-1994; 94US-00286846.  
 PR 20-DEC-1994; 94US-00359705.  
 XX (GETH ) GENENTECH INC.  
 PA Presta LG, Shelton DL, Urfer R;  
 PI WPI: 1995-344616/44.  
 XX N-PSDB; AAT00689.  
 DR  
 XX New human trkB and trkc poly-peptide(s) and fusion proteins contg. them -  
 PT also DNA, vectors and transformed cells useful in treatment and diagnosis  
 PT of abnormal neurotrophic factor expression, e.g. inflammatory pain.  
 XX  
 PS Claim 8; Fig 1A-B; 117bp; English.  
 CC This sequence may be expressed recombinantly for the production of human  
 CC trkB receptor, and to detect or amplify trkc genes. The encoded protein  
 CC may be used as a reagent in kinase receptor activation assays, and  
 CC therapeutically in diseases associated with over or under expression of  
 CC neurotrophic factor (e.g. pain of inflammation, kidney, lung,  
 CC cardiovascular or psychiatric disorders and some sorts of tumours). At  
 CC the indicated splice site, AA 436-791 may be replaced by the sequence  
 CC FVLFRKIPIDG (AAR81624)  
 CC  
 XX  
 SQ Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 2; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGGPAMRLMGFCMLVVGFWRAAFACPTSCSCSARJWCSPSPGIYAFPRLEP 60  
 DB 1 MSSWIRHGGPAMRLMGFCMLVVGFWRAAFACPTSCSCSARJWCSPSPGIYAFPRLEP 60  
 QY 61 NSVDPENITEIFIANQKRLIINEDDVEAYVGLNLTIVDSGLKFWAHKAFKXSNLOHI 120  
 DB 61 NSVDPENITEIFIANQKRLIINEDDVEAYVGLNLTIVDSGLKFWAHKAFKXSNLOHI 120  
 QY 121 NFRNKLITLSRKHFRHLDSBLILVGNPFTSCDINWIKTLOBAKSSPTDLYCLNES 180  
 DB 121 NFRNKLITLSRKHFRHLDSBLILVGNPFTSCDINWIKTLOBAKSSPTDLYCLNES 180  
 QY 181 SKNIPLANLOIPNCGLPANLAAANLTVBEGKSTTLCGVAADPVPMYMDVGNLVSKM 240  
 DB 181 SKNIPLANLOIPNCGLPANLAAANLTVBEGKSTTLCGVAADPVPMYMDVGNLVSKM 240  
 QY 241 NETSHTQGLRITNISGSDSGKOISCVARNLVGEDQSVMLTVFAFTITFLBSPSTDH 300  
 DB 241 NETSHTQGLRITNISGSDSGKOISCVARNLVGEDQSVMLTVFAFTITFLBSPSTDH 300  
 QY 301 WCIPFTVGNPKPALQWPFYNGAILNESKYICTKIHTNHTERYGCTQLDNPTHANNGBYT 360  
 DB 301 WCIPFTVGNPKPALQWPFYNGAILNESKYICTKIHTNHTERYGCTQLDNPTHANNGBYT 360  
 QY 361 LIANEKGKDEKQISAFPMGPGIDGAPNYPVYIYEDGTANODGDTTNSNEIPST 420  
 DB 361 LIANEKGKDEKQISAFPMGPGIDGAPNYPVYIYEDGTANODGDTTNSNEIPST 420  
 QY 421 DVTDKTRBHLASYAVVAVVIVSVGFCLLVMLFLKLARHSKFGKSGPASYISNDDDSASP 480  
 DB 421 DVTDKTRBHLASYAVVAVVIVSVGFCLLVMLFLKLARHSKFGKSGPASYISNDDDSASP 480  
 QY 481 LHHISNGSNTSSSGGPDVAVIIGMTKIPVLENQYFGITNSQLKPDTPVOHIKRANIYL 540  
 DB 481 LHHISNGSNTSSSGGPDVAVIIGMTKIPVLENQYFGITNSQLKPDTPVOHIKRANIYL 540  
 QY 541 KRELGBAEGKVFALACYNLCPEODKILVAVKTLKXASDNARKDFHREBELTNLOHEHI 600  
 DB 541 KRELGBAEGKVFALACYNLCPEODKILVAVKTLKXASDNARKDFHREBELTNLOHEHI 600

DB 541 KRELGBAEGKVFALACYNLCPEODKILVAVKTLKXASDNARKDFHREBELTNLOHEHI 600  
 QY 601 VKFYGVCSBGDPLIMVPEYMKHGDINKFLRAHPDPAVLAEGNPPTFLTOSQMLHIAQOI 660  
 DB 601 VKFYGVCSBGDPLIMVPEYMKHGDINKFLRAHPDPAVLAEGNPPTFLTOSQMLHIAQOI 660  
 QY 661 AAGMYVLASQHFVHRLATFNCLVGENLIVKIDPGMSRPVYSTDYRVGHTMLPIRMM 720  
 DB 661 AAGMYVLASQHFVHRLATFNCLVGENLIVKIDPGMSRPVYSTDYRVGHTMLPIRMM 720  
 QY 721 PPSIMTRKFTESDYSLSGVLMELFTYQKOPWYOLSNNVEICTQGRVLQRPRTCPQ 780  
 DB 721 PPSIMTRKFTESDYSLSGVLMELFTYQKOPWYOLSNNVEICTQGRVLQRPRTCPQ 780  
 QY 781 EYVELMGCMQRPBHRKNIKGIHTLLQNLAKASPVYLDILG 822  
 DB 781 EYVELMGCMQRPBHRKNIKGIHTLLQNLAKASPVYLDILG 822

## RESULT 2

AA51599  
 ID AAY51599 standard; protein; 822 AA.

XX AAY51599;

AC 30-MAY-2000 (first entry)

DE Human trkB receptor protein.

KM trkB; human; receptor tyrosine kinase; trkc; diagnosis; neurotrophin;

KW neurotrophic factor.

OS Homo sapiens.

PN US6027927-A.

PD 22-FEB-2000.

PF 01-OCT-1997; 97US-00942562.

XX 18-MAR-1994; 94US-00215139.

PR 05-AUG-1994; 94US-00286846.

PR 19-MAY-1995; 95US-00444597.

XX (GETH ) GENENTECH INC.

PI Urfer R, Shelton DL, Presta LG;

DR WPI: 2000-194832/17.

DR N-PSDB; AAZ88839.

PT New human trk receptors useful in the diagnosis of various human

PT pathological conditions associated with elevated or reduced levels of

PT neurotrophins capable of binding trkB and/or trkc.

PS Claim 1; Col 63-68; 78bp; English.

CC This invention describes a novel isolated and purified polypeptide (1),

CC belonging to the trk family of receptor tyrosine kinases, trks and trkc.

CC (1) are useful in the purification of human neurotrophic factors and in

CC the diagnosis of various human pathological conditions associated with

CC elevated or reduced levels of neurotrophins capable of binding trkB

CC and/or trkc. This sequence represents the human trkB receptor described

CC in the method of the invention

SO Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 3; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGGPAMRLMGFCMLVVGFWRAAFACPTSCSCSARJWCSPSPGIYAFPRLEP 60

Db 1 MSSWIRHGMARLNGRCMLVGFWRAPAFACPTSCSKSARIKWCSPSPGIVA PPRLEP 60  
 Qy 61 NSVDPENITTEIFIANQRLIEINEDVEAYVGLANLTI VDSGLKFAHKAFLKXSNLQHI 120  
 Db 61 NSVDPENITTEIFIANQRLIEINEDVEAYVGLANLTI VDSGLKFAHKAFLKXSNLQHI 120  
 Qy 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Db 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Qy 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Db 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Qy 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEGKSITLSCSVAGDVPNNYMDVGNLVSKM 240  
 Db 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEGKSITLSCSVAGDVPNNYMDVGNLVSKM 240  
 Qy 241 NETSHTQSLRITNIISSDSDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300  
 Db 241 NETSHTQSLRITNIISSDSDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300  
 Qy 301 WCIPFTYKGNPKPALQWFFNGAIIINESKICTKIHVTNHTYHGCLOLDNPTTHMNGDYT 360  
 Db 301 WCIPFTYKGNPKPALQWFFNGAIIINESKICTKIHVTNHTYHGCLOLDNPTTHMNGDYT 360  
 Qy 361 LIAKNEYGKQKQISAFPMGPGIDGAPNPNYVIEDGTANDIGDTTNRSENEIPST 420  
 Db 361 LIAKNEYGKQKQISAFPMGPGIDGAPNPNYVIEDGTANDIGDTTNRSENEIPST 420  
 Qy 421 DVTDKTGREHLSVYAVVVIASVVGFCLLVMLFLKLARHSKFGMKGPASVISNDSDASP 480  
 Db 421 DVTDKTGREHLSVYAVVVIASVVGFCLLVMLFLKLARHSKFGMKGPASVISNDSDASP 480  
 Qy 481 LIAHISNGSNTPSSSEGGPDAVIGMTKIPVIEINPQYFGITNSOLKPDTFVGHIRKHNIVL 540  
 Db 481 LIAHISNGSNTPSSSEGGPDAVIGMTKIPVIEINPQYFGITNSOLKPDTFVGHIRKHNIVL 540  
 Qy 541 KRELGEBAFGVYFLAECYNLCPEODKILVAVKTKLKDASDNARKDFHREAEILLTNLQHEHI 600  
 Db 541 KRELGEBAFGVYFLAECYNLCPEODKILVAVKTKLKDASDNARKDFHREAEILLTNLQHEHI 600  
 Qy 601 VKFPGVCEBGPDLNMFPEYMGHGLDKFLRAHGPDAVIMARGNPTELITQSOMLHIAQOI 660  
 Db 601 VKFPGVCEBGPDLNMFPEYMGHGLDKFLRAHGPDAVIMARGNPTELITQSOMLHIAQOI 660  
 Qy 661 AAGNVYIASQHFVARDLATRNCLVGENLVKIGDFGMSRDVYSTDYVVGSHITMLPIFKM 720  
 Db 661 AAGNVYIASQHFVARDLATRNCLVGENLVKIGDFGMSRDVYSTDYVVGSHITMLPIFKM 720  
 Qy 721 PPESIMYRKFTTESDVSLSGVLMWEIFTYGKQPMYQOLSNNVEICTTQGRVLORPRTCPQ 780  
 Db 721 PPESIMYRKFTTESDVSLSGVLMWEIFTYGKQPMYQOLSNNVEICTTQGRVLORPRTCPQ 780  
 Qy 781 EYVELMIGCQWQREPMRNKIKGIHTLONLAKASPVYDIIG 822  
 Db 781 EYVELMIGCQWQREPMRNKIKGIHTLONLAKASPVYDIIG 822  
 RESULT 3  
 AAE27931  
 ID AAE27931 standard; protein; 822 AA.  
 XX AAE27931;  
 AC 27-DEC-2002 (first entry)  
 DT  
 XX  
 DE Human TrkB protein.  
 XX Human; neurodegenerative disorder; neurodevelopmental disorder; TrkB;  
 KM TrkB; Alzheimer's disease; AD; amyotrophic lateral sclerosis; ALS; PD;  
 KM Parkinson's disease; Huntington's disease; HD; Lou Gehrig's disease;  
 KM diabetic peripheral neuropathy; Down's syndrome; DS; neuroprotective;  
 KM gene therapy; anticonvulsant; cerebroprotective; nootropic.  
 XX Homo sapiens.  
 OS  
 XX

PN W0200267858-A2.  
 XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-US005151.  
 XX 22-FEB-2001; 2001US-0270553P.  
 XX (UYMA-) UNIV MARYLAND BALTIMORE.  
 PA Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;  
 PI WPI; 2002-698627/75.  
 XX DR N-PSDB; AAD45786.  
 XX Treating and/or preventing neurodegenerative and neurodevelopmental  
 PT disorders such as Alzheimer's, Parkinson's and Huntington's diseases by  
 PT altering the ratio of amount of full-length and truncated TrkB or TrkC  
 PT polypeptides.  
 PS Claim 47; Page 56-59; 96pp; English.  
 XX The present invention relates to a method of treating neurodegenerative  
 CC or neurodevelopmental disorders in a mammal which involves administering  
 CC an isolated nucleic acid encoding a full-length TrkB or TrkC or their  
 CC mutant, variant, homologue or fragment or an anti-sense RNA for truncated  
 CC TrkB or TrkC isoforms, where they increase the amount of full-length TrkB  
 CC or TrkC or decrease the amount of truncated TrkB or TrkC in treated  
 CC neurons. The methods and compositions of the invention are useful for  
 CC treating or preventing neurodegenerative or neurodevelopmental disorders  
 CC such as Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's  
 CC disease (HD), amyotrophic lateral sclerosis (ALS), Lou Gehrig's disease,  
 CC diabetic peripheral neuropathy, the adverse complications of Down's  
 CC syndrome (DS) and other types of peripheral neuropathy. Sequences of the  
 CC invention are also used in gene therapy. The present sequence is human  
 CC TrkB protein  
 XX  
 SQ Sequence 822 AA;  
 Query Match 100.0%; Score 4419; DB 5; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSSWIRHGMARLNGRCMLVGFWRAPAFACPTSCSKSARIKWCSPSPGIVA PPRLEP 60  
 Db 1 MSSWIRHGMARLNGRCMLVGFWRAPAFACPTSCSKSARIKWCSPSPGIVA PPRLEP 60  
 Qy 61 NSVDPENITTEIFIANQRLIEINEDVEAYVGLANLTI VDSGLKFAHKAFLKXSNLQHI 120  
 Db 61 NSVDPENITTEIFIANQRLIEINEDVEAYVGLANLTI VDSGLKFAHKAFLKXSNLQHI 120  
 Qy 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Db 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Qy 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Db 121 NPTNKLTSLSRKFRHLDSELLVGNPFCCSDIMWIKTLQAKSPPTQDLYCLNES 180  
 Qy 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEGKSITLSCSVAGDVPNNYMDVGNLVSKM 240  
 Db 181 SKNIPLANLOIPNCGLSANLAAPNLTVBEGKSITLSCSVAGDVPNNYMDVGNLVSKM 240  
 Qy 241 NETSHTQSLRITNIISSDSDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300  
 Db 241 NETSHTQSLRITNIISSDSDSGKQISCAVENLVGEDODSVNLTVHAPPTITLESPTSDDH 300  
 Qy 301 WCIPFTYKGNPKPALQWFFNGAIIINESKICTKIHVTNHTYHGCLOLDNPTTHMNGDYT 360  
 Db 301 WCIPFTYKGNPKPALQWFFNGAIIINESKICTKIHVTNHTYHGCLOLDNPTTHMNGDYT 360  
 Qy 361 LIAKNEYGKQKQISAFPMGPGIDGAPNPNYVIEDGTANDIGDTTNRSENEIPST 420  
 Db 361 LIAKNEYGKQKQISAFPMGPGIDGAPNPNYVIEDGTANDIGDTTNRSENEIPST 420  
 Qy 421 DVTDKTGREHLSVYAVVVIASVVGFCLLVMLFLKLARHSKFGMKGPASVISNDSDASP 480  
 Db 421 DVTDKTGREHLSVYAVVVIASVVGFCLLVMLFLKLARHSKFGMKGPASVISNDSDASP 480

Db 421 DVTDKTGRHLVSYAVVVIASVGFCLLWMLFLIKLARHSKFGKGPASVISNDSDSASP 480  
 QY 481 LHHISNGSNTSSSESGPDAVIGMTKIPVLENPQYGTNSQAKPPTFYQHIKRHNI VL 540  
 Db 481 LHHISNGSNTSSSESGPDAVIGMTKIPVLENPQYGTNSQAKPPTFYQHIKRHNI VL 540  
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 Db 541 KRELGEBAFGKVFIAECYNLCPEODKILVAVKTLKQASDNARKDFHREABILLNLQHEHT 600  
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 Db 601 VKFYGVCEBGDPLIMVEFYMKHGDLNKEFLRAHGDAVLMAGNPPTLSTOSMLHIAQOI 660  
 QY 661 AAGVYVLAHQFVHRDLATRNCLVGENILVYKIGDPGNSRDVYSTDYRYRGHTMLPIRM 720  
 Db 661 AAGVYVLAHQFVHRDLATRNCLVGENILVYKIGDPGNSRDVYSTDYRYRGHTMLPIRM 720  
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 Db 721 PPESIMYRKTTTSDVWSLGVLTWEITTYGKQPYQLSNNEVIECTQGRVLOKPTCPQ 780  
 QY 781 EYVELMIGCWOREPHMKNTKGIHTLLONLAKSPVYLDILG 822  
 Db 781 EYVELMIGCWOREPHMKNTKGIHTLLONLAKSPVYLDILG 822

## RESULT 4

AAM50851  
 ID AAM50851 standard; protein; 822 AA.

AC AAM50851;

DT 01-MAY-2002 (first entry)

XX Human receptor tyrosine kinase TrkB.

XX Receptor tyrosine kinase; TrkB; receptor; human;

KM brain derived growth factor; BDNF; neurotrophin-3; NT-3;

KM Huntington's disease; Parkinson's disease; Alzheimer's disease;

KM amyotrophic lateral sclerosis; neurodegenerative disease; cancer;

KM neuroprotective; nootropic; anticonvulsant; antiparkinsonian; enzyme;

KM cytoskeletal; therapy.

XX Homo sapiens.

OS

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Key Location/Qualifiers  
 Peptide 1..31  
 Protein /label= Signal\_peptide  
 32..822  
 Domain /label= Mature\_protein  
 32..430  
 Modified-site /label= Extracellular  
 67  
 Domain /note= "N-glycosylated"  
 72..117  
 Region /label= Leucine-rich\_repeats  
 72..93  
 Modified-site /note= "leucine-rich repeat 1"  
 95  
 Region /note= "N-glycosylated"  
 96..117  
 Modified-site /note= "leucine-rich repeat 2"  
 121  
 Modified-site /note= "N-glycosylated"  
 178  
 Modified-site /note= "N-glycosylated"  
 205  
 Domain /note= "N-glycosylated"  
 214..270  
 Modified-site /label= Ig-like\_C2-type  
 241  
 /note= "N-glycosylated"

FT Modified-site 254  
 FT /note= "N-glycosylated"  
 FT Modified-site 280  
 FT /note= "N-glycosylated"  
 FT Domain 301..365  
 FT /label= Ig-like\_C2-type  
 FT Modified-site 325  
 FT /note= "N-glycosylated"  
 FT Modified-site 338  
 FT /note= "N-glycosylated"  
 FT Modified-site 412  
 FT /note= "N-glycosylated"  
 FT Domain 431..454  
 FT /label= Transmembrane  
 FT Domain 455..822  
 FT /label= Cytoplasmic  
 FT Misc-difference 467..477  
 FT /note= "replaced by FULFKRIPLDG is truncated isoform"  
 FT Misc-difference 478..822  
 FT /note= "missing in truncated isoform"  
 FT Binding-site 516  
 FT /note= "interaction with SHC protein"  
 FT Modified-site 516  
 FT /note= "O-phosphorylated"  
 FT Domain 538..807  
 FT /label= Protein\_kinase  
 FT Region 544..552  
 FT /note= "ATP binding site"  
 FT Region 572  
 FT /note= "ATP binding site"  
 FT Active-site 676  
 FT Modified-site 702  
 FT /note= "O-phosphorylated"  
 FT Modified-site 706  
 FT /note= "O-phosphorylated"  
 FT Modified-site 707  
 FT /note= "O-phosphorylated"  
 FT Binding-site 817  
 FT /note= "interaction with PLC-gamma-1"  
 FT Modified-site 817  
 FT /note= "O-phosphorylated"  
 FT  
 PN WO200203071-A2.  
 XX  
 XX 10-JAN-2002.  
 XX  
 PF 05-JUL-2001; 2001MO-US021472.  
 XX  
 XX 05-JUL-2000; 2000US-0215778P.  
 XX  
 PA (PANG-) PANGENE CORP.  
 PI  
 PI Bates AT;  
 XX  
 XX WPI; 2002-179638/23.  
 DR  
 XX Screening for a neurotrophic factor mimetic, useful for treating, e.g.,  
 PT cancer and Alzheimer's, comprises combining a candidate mimetic with a  
 PT fragment of a tyrosine kinase protein.  
 PT  
 XX  
 PS Disclosure; Fig 11A; 107pp; English.  
 XX  
 CC The present sequence is that of human receptor tyrosine kinase TrkB, the  
 CC receptor for brain-derived growth factor (BDNF) and neurotrophin-3 (NT-  
 CC 3). The invention concerns Trks and their ligands that modulate cell  
 CC growth, differentiation and survival. Trk proteins are known to mediate  
 CC the activities of neurotrophins and are also known proto-oncogenes.  
 CC Methods are claimed for screening for small molecule neurotrophic factor  
 CC (NTP) mimetics, such as the cyclic peptide given in AAM50844, capable of  
 CC binding to a Trk protein or of modulating the binding of a neurotrophin  
 CC to a Trk protein. Also claimed are medicaments comprising a small  
 CC molecule NTP mimetic and their use in claimed methods for treatment of  
 CC cancer or a neurodegenerative disease selected from Huntington's disease,



CC Parkinson's disease, Alzheimer's disease and amyotrophic lateral sclerosis  
 CC  
 XX  
 XX

Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 5; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGPAMALMGFCMLVGFWRAPAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60  
 DB 1 MSSWIRHGPAMALMGFCMLVGFWRAPAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60  
 QY 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120  
 DB 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120  
 QY 121 NFTNKLTSLSRKHFRLDLSELILVGNPFTCSQIMWIKTLQBAKSSPTQDLYCLNES 180  
 DB 121 NFTNKLTSLSRKHFRLDLSELILVGNPFTCSQIMWIKTLQBAKSSPTQDLYCLNES 180  
 QY 181 SKNPLANLOIPNCGLPANLAAPNLTEEGKSITLSCVAGDPVPMNYMDVGNLVSKM 240  
 DB 181 SKNPLANLOIPNCGLPANLAAPNLTEEGKSITLSCVAGDPVPMNYMDVGNLVSKM 240  
 QY 241 NETSHTQSLRITNISSDSGKOISCVANLVGEDODSVNLTVHAPPTITLESPTSQDH 300  
 DB 241 NETSHTQSLRITNISSDSGKOISCVANLVGEDODSVNLTVHAPPTITLESPTSQDH 300  
 QY 301 WCIPFTVGNKPKPALQWFTNGAILNESKYICTKIHVTNHTHYGCLQIDNPTMANNQDYT 360  
 DB 301 WCIPFTVGNKPKPALQWFTNGAILNESKYICTKIHVTNHTHYGCLQIDNPTMANNQDYT 360  
 QY 361 LIAKNEYKDKKOISAHFMWPGIDDGANPNYPIYDYCTAANDIGDTNRSENEIPST 420  
 DB 361 LIAKNEYKDKKOISAHFMWPGIDDGANPNYPIYDYCTAANDIGDTNRSENEIPST 420  
 QY 421 DVTDKTGREHLSYAVVVIASVGFCLVLMFLKLARHSFKMGKGPASVISNDDSGSP 480  
 DB 421 DVTDKTGREHLSYAVVVIASVGFCLVLMFLKLARHSFKMGKGPASVISNDDSGSP 480  
 QY 481 LHHISNSGNTSPSSSEGGDAVIGMTKIPVIEENPQYFGITNSQLKPDTFVOHKKRNLVL 540  
 DB 481 LHHISNSGNTSPSSSEGGDAVIGMTKIPVIEENPQYFGITNSQLKPDTFVOHKKRNLVL 540  
 QY 541 KRELGEAGFGVFLAECYNLCPEODKILVAVKTLKDSADNARKDFHRAEALLTNLOHEHI 600  
 DB 541 KRELGEAGFGVFLAECYNLCPEODKILVAVKTLKDSADNARKDFHRAEALLTNLOHEHI 600  
 QY 601 VKFPGVCVBGDPPLIMVFEMHGDLNKFLEAHGPDVLMAGNPPTELTOSOMLHIAQOI 660  
 DB 601 VKFPGVCVBGDPPLIMVFEMHGDLNKFLEAHGPDVLMAGNPPTELTOSOMLHIAQOI 660  
 QY 661 AAGVNYLASQHFVARDLATRNCLVGENLVKIGDFGMSRDYSTDYRVVGHITMLPIKRM 720  
 DB 661 AAGVNYLASQHFVARDLATRNCLVGENLVKIGDFGMSRDYSTDYRVVGHITMLPIKRM 720  
 QY 721 PPBSIMTRKFTTESDWSLSGVYLWEIFTYGQPMYQOLSNNVEICTTQGRVLOQRPTCPQ 780  
 DB 721 PPBSIMTRKFTTESDWSLSGVYLWEIFTYGQPMYQOLSNNVEICTTQGRVLOQRPTCPQ 780  
 QY 781 EYVELMIGCQWOREPHMRKNIGIHITLONLAKASPVYDIIG 822  
 DB 781 EYVELMIGCQWOREPHMRKNIGIHITLONLAKASPVYDIIG 822

RESULT 5  
 ID ABUS6698 standard; protein; 822 AA.  
 AC ABUS6698;  
 XX

DT 02-APR-2003 (first entry)

XX Lung cancer-associated polypeptide #291.  
 DE  
 XX  
 XX  
 KW Lung cancer-associated polypeptide; cytosolic; emphysema;  
 KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX  
 OS Unidentified.  
 XX  
 XX W0200286443-A2.  
 EN  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX 18-APR-2002; 2002WO-US012476.  
 PF  
 XX 18-APR-2001; 2001US-0284770P.  
 PR 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-0334370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Aziz N, Murray R;  
 XX WPI, 2003-093161/08.  
 DR N-PSDB; ABX76427.  
 DR  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 PT  
 PS Claim 27; Page 417-418; 453pp; English.  
 XX  
 XX The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridizes  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the  
 CC invention  
 CC  
 XX  
 XX Sequence 822 AA;  
 SQ  
 Query Match 100.0%; Score 4419; DB 6; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGPAMALMGFCMLVGFWRAPAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60  
 DB 1 MSSWIRHGPAMALMGFCMLVGFWRAPAFACPTSCCKSASRIMCSDPSPGIVAFPRLEP 60  
 QY 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120  
 DB 61 NSVDPENITEIFIANOKRLIINEDDVEAYVGLNLTIVDSGLKFAVHAKAFKXSNLOHI 120  
 QY 121 NFTNKLTSLSRKHFRLDLSELILVGNPFTCSQIMWIKTLQBAKSSPTQDLYCLNES 180

Db 121 NFRNKLTSLSRKHFRHLDSEILVGNPPTCSDIMITLQBAKSSPTODLYCINES 180  
Qy 181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSAVAGPVPMMYDVGNLYSKM 240  
Db 181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSAVAGPVPMMYDVGNLYSKM 240  
Qy 241 NETSHTOGSLRITNISSDSGSKQISCAVENLVGEDDSVNLTVFAPTITFLSPISDHH 300  
Db 241 NETSHTOGSLRITNISSDSGSKQISCAVENLVGEDDSVNLTVFAPTITFLSPISDHH 300  
Qy 301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHTNHTETHGCLQDLPHTMNNDDYT 360  
Db 301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHTNHTETHGCLQDLPHTMNNDDYT 360  
Qy 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVIYEDYGTANDIGDTTNSNEIPST 420  
Db 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVIYEDYGTANDIGDTTNSNEIPST 420  
Qy 421 DVTDKTGREHLASYAVAVVIVASVGFCLVNLFLIKLARSHKFGMKGPASVISNDDBASP 480  
Db 421 DVTDKTGREHLASYAVAVVIVASVGFCLVNLFLIKLARSHKFGMKGPASVISNDDBASP 480  
Qy 481 LHHISNGSNTSSSEGGPDVITIGMTKIPVTEHPQYFGITNSQKXPTFQHIKRNHIVL 540  
Db 481 LHHISNGSNTSSSEGGPDVITIGMTKIPVTEHPQYFGITNSQKXPTFQHIKRNHIVL 540  
Qy 541 KRELBSGAFGKFLAECYNLCPEBODKILVAVKTLKADSDNARKDPRHREASILLTLOHEHI 600  
Db 541 KRELBSGAFGKFLAECYNLCPEBODKILVAVKTLKADSDNARKDPRHREASILLTLOHEHI 600  
Qy 601 VKFPGVCEBGPLIMVEYEMKRGDLNFKLRAHGDVAVLMEGNPTELITQSMHIAQOI 660  
Db 601 VKFPGVCEBGPLIMVEYEMKRGDLNFKLRAHGDVAVLMEGNPTELITQSMHIAQOI 660  
Qy 661 AAGVNYLASQHFVRDLATRNCLVGENLVKIGDFGMSRDYSDYYRVGSHMLPIRRM 720  
Db 661 AAGVNYLASQHFVRDLATRNCLVGENLVKIGDFGMSRDYSDYYRVGSHMLPIRRM 720  
Qy 721 PPSISIMTRKFTTESDVMSLGVLMIEFTYQKOPYQOLSNNVEIECITQGRVLAQRPTCPQ 780  
Db 721 PPSISIMTRKFTTESDVMSLGVLMIEFTYQKOPYQOLSNNVEIECITQGRVLAQRPTCPQ 780  
Qy 781 EYVELMIGCWOREPHMRKNIKGIHTLQNLAKASPVYIDLIG 822  
Db 781 EYVELMIGCWOREPHMRKNIKGIHTLQNLAKASPVYIDLIG 822

RESULT 6  
ABR82949 standard; protein; 822 AA.  
ID ABR82949;  
AC ABR82949;  
XX 18-DEC-2003 (first entry)  
DT 18-DEC-2003 (first entry)  
XX Human TrkB polypeptide.  
DE Human TrkB polypeptide.  
XX TrkB; TrkC; neurodegenerative; neuro-developmental; antiparkinsonian;  
KM neuroprotective; anticonvulsant; cerebroprotective; vasotropic;  
KN neurotrophic; human.  
XX Homo sapiens.  
OS Homo sapiens.  
XX MO2003071872-A1.  
PN MO2003071872-A1.  
XX 04-SEP-2003.  
XX 28-MAY-2002; 2002WO-US016807.  
PF 22-FEB-2002; 2002WO-US005151.  
PR (UTMA-) UNIV MARYLAND BALTIMORE.  
XX PA

PA (KRUE/) KRUEGER B K.  
PA (KING/) KINGSBURY T J.  
PA (BAMB/) BAMBRICK L L.  
PA (DORS/) DORSEY S G.  
XX  
PI Kuenger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;  
XX WPI, 2003-731549/69.  
DR N-PSDB; ACF36565.  
XX  
PT Treating and/or preventing neurodegenerative or neuro-developmental  
PT disorders, such as Alzheimer's disease, Parkinson's disease and  
PT amyotrophic lateral sclerosis, using nucleic acids encoding TrkB and/or  
PT TrkB polypeptides.  
XX  
XX Claim 47; Page 58-61; 99pp; English.  
XX  
CC The invention relates to treating a neurodegenerative or neuro-  
CC developmental disorder in a mammal. The method involves altering the  
CC ratio of the amount of full length TrkB polypeptide to the amount of  
CC truncated TrkB polypeptides in a neuron or by altering the ratio of the  
CC amount of full length TrkB polypeptide to the amount of truncated TrkB  
CC polypeptides in a neuron. The methods and compositions of the present  
CC invention are useful for treating and/or preventing a neurodegenerative  
CC or neuro-developmental disorder, such as Alzheimer's disease, Parkinson's  
CC disease, Huntington's disease, amyotrophic lateral sclerosis (Lou  
CC Gehrig's disease), the adverse neurologic complications of Down syndrome,  
CC diabetic peripheral neuropathy and other types of peripheral neuropath,  
CC and is associated with an injury to the central or peripheral nervous  
CC system resulting from stroke, cerebral ischaemia, or chemical and/or  
CC physical trauma. The present sequence represents a human TrkB polypeptide  
CC (Genbank Accession No. NM\_006180)  
XX  
SQ Sequence 822 AA;  
Query Match 100.0%; Score 4419; DB 7; Length 822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSSMIRHNGPAMRLNGFCWLIVGFMRAPACPTSCKSASRIWCSDPSPGIVAFPLEP 60  
Db 1 MSSMIRHNGPAMRLNGFCWLIVGFMRAPACPTSCKSASRIWCSDPSPGIVAFPLEP 60  
Qy 61 NSVDPENITEIFIANQRLIEINEDVEAYVGRNLTIVDSGLKFAVAKAFKNSNIQHT 120  
Db 61 NSVDPENITEIFIANQRLIEINEDVEAYVGRNLTIVDSGLKFAVAKAFKNSNIQHT 120  
Qy 121 NFRNKLTSLSRKHFRHLDSEILVGNPPTCSDIMITLQBAKSSPTODLYCINES 180  
Db 121 NFRNKLTSLSRKHFRHLDSEILVGNPPTCSDIMITLQBAKSSPTODLYCINES 180  
Qy 181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSAVAGPVPMMYDVGNLYSKM 240  
Db 181 SKNIPLANLOIPNCGPSANLAAPNLTVBEGKSITLSCSAVAGPVPMMYDVGNLYSKM 240  
Qy 241 NETSHTOGSLRITNISSDSGSKQISCAVENLVGEDDSVNLTVFAPTITFLSPISDHH 300  
Db 241 NETSHTOGSLRITNISSDSGSKQISCAVENLVGEDDSVNLTVFAPTITFLSPISDHH 300  
Qy 301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHTNHTETHGCLQDLPHTMNNDDYT 360  
Db 301 WCIPFTYKGNPKPALQMFYNGALINBSKYICTKIHTNHTETHGCLQDLPHTMNNDDYT 360  
Qy 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVIYEDYGTANDIGDTTNSNEIPST 420  
Db 361 LIANNEYGKDEKQISAHFMGPGIDGAPNYPDVIYEDYGTANDIGDTTNSNEIPST 420  
Qy 421 DVTDKTGREHLASYAVAVVIVASVGFCLVNLFLIKLARSHKFGMKGPASVISNDDBASP 480  
Db 421 DVTDKTGREHLASYAVAVVIVASVGFCLVNLFLIKLARSHKFGMKGPASVISNDDBASP 480  
Qy 481 LHHISNGSNTSSSEGGPDVITIGMTKIPVTEHPQYFGITNSQKXPTFQHIKRNHIVL 540  
Db 481 LHHISNGSNTSSSEGGPDVITIGMTKIPVTEHPQYFGITNSQKXPTFQHIKRNHIVL 540

Db 481 LHHISNGSNTSPSSSEGGDAVIIGMTKIPVLENPOYFGITNSQLKPDPTFVOHIRHNIVL 540  
Qy 541 KRELGEBAFGKVPFLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTLQHNEHI 600  
Db 541 KRELGEBAFGKVPFLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTLQHNEHI 600  
Qy 601 VKFYGVCEGDPPLIMVFETMKHGDINKFLRAHGPDAVLMAGNPPTTELTOGMLHIAQOI 660  
Db 601 VKFYGVCEGDPPLIMVFETMKHGDINKFLRAHGPDAVLMAGNPPTTELTOGMLHIAQOI 660  
Qy 661 AAGNVYLASQHFVHRDLATRNCLVGENLLVKIGFGMSRDVYSIDYRVGHTMLPIRMM 720  
Db 661 AAGNVYLASQHFVHRDLATRNCLVGENLLVKIGFGMSRDVYSIDYRVGHTMLPIRMM 720  
Qy 721 PPESIMTRKFTTESDVMISGLVVLWEIFTYGGKQPMYQLSNNEVICITQGRVLQRPRTCPQ 780  
Db 721 PPESIMTRKFTTESDVMISGLVVLWEIFTYGGKQPMYQLSNNEVICITQGRVLQRPRTCPQ 780  
Qy 781 EVELMIGCWQREPHMRKNIGIHTLLQNLAKASPVYIDLIG 822  
Db 781 EVELMIGCWQREPHMRKNIGIHTLLQNLAKASPVYIDLIG 822

RESULT 7  
ADE40445

ID ADE40445 standard; protein; 822 AA.

AC ADE40445;

DT 29-JAN-2004 (first entry)

DE Human receptor tyrosine kinase TRKB (gene ID 5816) protein.

XX AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;  
KM HIV-related disorder; differential expression; drug screening;  
KM viral replication modulation; diagnosis; prognosis; predisposition;  
KM anti-HIV; gene therapy; antisense therapy; human;  
XX receptor tyrosine kinase TRKB; enzyme.

XX Homo sapiens.

XX W02003070883-A2.

XX 28-AUG-2003.

XX 13-FEB-2003; 2003WO-US004246.

XX 15-FEB-2002; 2002US-0357391P.

XX 13-MAY-2002; 2002US-0380249P.

XX 25-JUN-2002; 2002US-0391306P.

XX 27-AUG-2002; 2002US-0406297P.

XX 19-SEP-2002; 2002US-0412007P.

XX 10-OCT-2002; 2002US-0417508P.

XX 10-DEC-2002; 2002US-0432318P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Powell DM, Weich NS;

XX WPI; 2003-671808/63.

XX N-PSDB; ADE40444.

XX Identifying a compound capable of diagnosing, preventing or treating AIDS

XX or an HIV-related disorder comprises assaying the ability of the compound

XX to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or

XX polypeptide activity.

XX Claim 1; SEQ ID NO 24; 167bp; English.

CC 26 human proteins. These proteins and nucleic acids encoding them  
CC (ADE40422-ADE40473) are differentially expressed in tissues relating to  
CC AIDS or an HIV-related disorder compared to their expression in normal  
CC tissues. The invention also relates to the use of the compounds  
CC identified to modulate viral replication in a cell and to treat a patient  
CC with AIDS or an HIV-related disorder. The invention further discloses  
CC methods for the diagnostic evaluation and prognosis of various HIV-  
CC related disorders, and for the identification of individuals exhibiting a  
CC predisposition to such conditions. The modulatory compounds identified  
CC using the method of the invention may be small organic molecules,  
CC peptides, antibodies or antisense nucleic acid molecules. The methods of  
CC the invention are useful in diagnosing, preventing or treating AIDS or  
CC HIV-related disorders. The present sequence represents a human protein  
CC which is differentially expressed in AIDS or HIV-related disorders.

SQ Sequence 822 AA;

Query Match 100.0%; Score 4419; DB 7; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSWIRHGPAMARLWGCWLVGFMRAAFACPTSCSCASRIWCPDPSPGIVAAPPREP 60  
Db 1 MSSWIRHGPAMARLWGCWLVGFMRAAFACPTSCSCASRIWCPDPSPGIVAAPPREP 60  
Qy 61 NSVDPENITTEIFIANOKRLIETINEDVEAYVGLNLTIVDSGLKFVAHKAFLKSNLQHI 120  
Db 61 NSVDPENITTEIFIANOKRLIETINEDVEAYVGLNLTIVDSGLKFVAHKAFLKSNLQHI 120  
Qy 121 NFRNKLTSLSRKAFRHLDELILVGNPPTGSCDINWIKTLQFAKSSPTDLYCLNES 180  
Db 121 NFRNKLTSLSRKAFRHLDELILVGNPPTGSCDINWIKTLQFAKSSPTDLYCLNES 180  
Qy 181 SKNPLANLQIPNGLGSANLAAAPNLVBEBSKLTLSGSVAGDPVPMYVGNLVSGM 240  
Db 181 SKNPLANLQIPNGLGSANLAAAPNLVBEBSKLTLSGSVAGDPVPMYVGNLVSGM 240  
Qy 241 NETSHTQSLRITNIISSDDSGKQISVAENLVGEDDSVNLTVFAPTITLESPTSDDH 300  
Db 241 NETSHTQSLRITNIISSDDSGKQISVAENLVGEDDSVNLTVFAPTITLESPTSDDH 300  
Qy 241 NETSHTQSLRITNIISSDDSGKQISVAENLVGEDDSVNLTVFAPTITLESPTSDDH 300  
Db 241 NETSHTQSLRITNIISSDDSGKQISVAENLVGEDDSVNLTVFAPTITLESPTSDDH 300  
Qy 301 WCIPFTVKNPKPALQFNGAILNESKYICTKIHTNHTYHGCLOLDNPTNNGDYT 360  
Db 301 WCIPFTVKNPKPALQFNGAILNESKYICTKIHTNHTYHGCLOLDNPTNNGDYT 360  
Qy 361 LIAKNEYGKDEKQISAFPMGPGIDGAPNYPVYIYEDYGTANDIGDITNRSNEIPST 420  
Db 361 LIAKNEYGKDEKQISAFPMGPGIDGAPNYPVYIYEDYGTANDIGDITNRSNEIPST 420  
Qy 421 DVTDKTRERHLSYAAVVVIVASVGFCLVLMFLKLRHSFKGKGPASVTSNDDDSASP 480  
Db 421 DVTDKTRERHLSYAAVVVIVASVGFCLVLMFLKLRHSFKGKGPASVTSNDDDSASP 480  
Qy 481 LHHISNGSNTSPSSSEGGDAVIIGMTKIPVLENPOYFGITNSQLKPDPTFVOHIRHNIVL 540  
Db 481 LHHISNGSNTSPSSSEGGDAVIIGMTKIPVLENPOYFGITNSQLKPDPTFVOHIRHNIVL 540  
Qy 541 KRELGEBAFGKVPFLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTLQHNEHI 600  
Db 541 KRELGEBAFGKVPFLAECYNLCPEODKILVAVKTKLSDASDNARKDFHREAEILLTLQHNEHI 600  
Qy 601 VKFYGVCEGDPPLIMVFETMKHGDINKFLRAHGPDAVLMAGNPPTTELTOGMLHIAQOI 660  
Db 601 VKFYGVCEGDPPLIMVFETMKHGDINKFLRAHGPDAVLMAGNPPTTELTOGMLHIAQOI 660  
Qy 661 AAGNVYLASQHFVHRDLATRNCLVGENLLVKIGFGMSRDVYSIDYRVGHTMLPIRMM 720  
Db 661 AAGNVYLASQHFVHRDLATRNCLVGENLLVKIGFGMSRDVYSIDYRVGHTMLPIRMM 720  
Qy 721 PPESIMTRKFTTESDVMISGLVVLWEIFTYGGKQPMYQLSNNEVICITQGRVLQRPRTCPQ 780  
Db 721 PPESIMTRKFTTESDVMISGLVVLWEIFTYGGKQPMYQLSNNEVICITQGRVLQRPRTCPQ 780

QY 781 EYEELMGCWQREBPHMRKNIKGHTLLQNLAKASPVYLDILG 822  
DB 781 EYEELMGCWQREBPHMRKNIKGHTLLQNLAKASPVYLDILG 822

RESULT 8  
ADN39076 ID ADN39076 standard; protein, 822 AA.

AC ADN39076;  
XX 17-JUN-2004 (first entry)  
XX 17-JUN-2004 (first entry)  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:394.

XX Human, differential expression; cancer; angiogenic disorder;  
KM fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KM inflammatory disease; autoimmune disease;  
KM retinal neovascularization syndrome; scarring; uterine fibroid;  
KM detection; diagnosis; prognosis; drug screening; drug targeting;  
KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
KM vulnery; gene therapy; vaccine.

XX Homo sapiens.  
OS  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PF 13-NOV-2002; 2002WO-US036610.

PR 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-0332464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0368099P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUN-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.

XX (BOSB-) BOS BIOTECHNOLOGY INC.  
PA  
PI Afez D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezl PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
XX WPI; 2003-468649/44.  
DR N-PSDB; ADN39075.

XX Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO 394; 1385PD; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.

XX  
XX Sequence 822 AA;  
SQ

Query Match 100.0%; Score 4419; DB 7; Length 822;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRNHPGAMRLMGCWLVGFWBAFAFACPTSCCKSASRIWCSPPGIVAFPLEP 60  
DB 1 MSSWIRNHPGAMRLMGCWLVGFWBAFAFACPTSCCKSASRIWCSPPGIVAFPLEP 60

QY 61 NSYDPEITITFIANQKRLIINEDDYBAVGLRNLTIYDSGLKFAVHKAFLKNSNIQHI 120  
DB 61 NSYDPEITITFIANQKRLIINEDDYBAVGLRNLTIYDSGLKFAVHKAFLKNSNIQHI 120

QY 121 NPTRNKLTLSRKHFRHLDSEILVGNPFTSCDIMWITKLOAKSPPTODLYCLNES 180  
DB 121 NPTRNKLTLSRKHFRHLDSEILVGNPFTSCDIMWITKLOAKSPPTODLYCLNES 180

QY 181 SKNIPLANLOIPNCGLPISANLAAPNLVEBGSITLSCSVAADPVPMMYDVGNLVSKM 240  
DB 181 SKNIPLANLOIPNCGLPISANLAAPNLVEBGSITLSCSVAADPVPMMYDVGNLVSKM 240

QY 241 NETSHTQSLRITNISSDGSCKOISYAEMLVGHODQSVNLTFHAPATTFLSPSTDDH 300  
DB 241 NETSHTQSLRITNISSDGSCKOISYAEMLVGHODQSVNLTFHAPATTFLSPSTDDH 300

QY 301 MCIPFTYKGNPKPALQFNYGAILNESKYCTKHVNHTEBYGCLQDNPTHMNGDYT 360  
DB 301 MCIPFTYKGNPKPALQFNYGAILNESKYCTKHVNHTEBYGCLQDNPTHMNGDYT 360

QY 361 LIAKNEYGDKDEKQISAFHFMWPGIDGANDPNYPVIEYEDYTAANDIGDTTNSNEIPST 420  
DB 361 LIAKNEYGDKDEKQISAFHFMWPGIDGANDPNYPVIEYEDYTAANDIGDTTNSNEIPST 420

QY 421 DVTDKTGRHLSYAAVVVYASVVGFCILVNLFLIKLARHSGFGKGPASVYSNDDDSASP 480  
DB 421 DVTDKTGRHLSYAAVVVYASVVGFCILVNLFLIKLARHSGFGKGPASVYSNDDDSASP 480

QY 481 LHHISNGSNTPSSSEGGPDVITIGMTKIPVIEHQYFGITNSOLKRPDPQHIRHNIVL 540  
DB 481 LHHISNGSNTPSSSEGGPDVITIGMTKIPVIEHQYFGITNSOLKRPDPQHIRHNIVL 540

QY 541 KRELGEAPGKVFLLAECYNLCPEODKILVAVKTLKSDANARKDFHRESELITVLAQEH 600  
DB 541 KRELGEAPGKVFLLAECYNLCPEODKILVAVKTLKSDANARKDFHRESELITVLAQEH 600

QY 601 VKFYGVCEBDDPLIMVEYKMGDLNFKFLRAHGDVAIVLMEAGNPPTBLTOSQMLHIAQOI 660  
DB 601 VKFYGVCEBDDPLIMVEYKMGDLNFKFLRAHGDVAIVLMEAGNPPTBLTOSQMLHIAQOI 660

QY 661 AAGGVYTLASQHPVHRDLATNCLVGENLLYKIDPFGMSRIVYSIDYRVGHTMLPIRMM 720  
DB 661 AAGGVYTLASQHPVHRDLATNCLVGENLLYKIDPFGMSRIVYSIDYRVGHTMLPIRMM 720

QY 721 PPSISIMYRKFTTESDVVSLGVLLMEITFYGKQPPYQOLSNNVEICTQGVLOQRPCTCPQ 780  
DB 721 PPSISIMYRKFTTESDVVSLGVLLMEITFYGKQPPYQOLSNNVEICTQGVLOQRPCTCPQ 780

QY 781 EYEELMGCWQREBPHMRKNIKGHTLLQNLAKASPVYLDILG 822  
DB 781 EYEELMGCWQREBPHMRKNIKGHTLLQNLAKASPVYLDILG 822

RESULT 9

ADN39954  
ID ADN39954 standard; protein; 822 AA.  
XX  
AC ADN39954;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C324.  
XX  
KM Human; differential expression; cancer; angiogenic disorder;  
KM fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KM inflammatory disease; autoimmune disease;  
KM retinal neovascularization syndrome; scarring; uterine fibroid;  
KM detection; diagnosis; prognosis; drug screening; drug targeting;  
KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
KM vulnery; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PF 13-NOV-2002; 2002W0-US036810.  
XX  
PR 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-0332464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335944P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0368809P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX  
PA (BOSB-) BOS BIOTECHNOLOGY INC.  
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Heyezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Ziornik A;  
XX  
DR WPI; 2003-468649/44.  
DR N-PSDB; ADN39737.  
XX  
PT Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
XX a nucleic acid in a biological sample.  
XX  
PS Claim 12; SEQ ID NO C324; 1385bp; English.  
XX  
XX The invention relates to nucleic acids and proteins (ADN38663-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.  
XX  
SQ Sequence 822 AA;  
Query Match 100.0%; Score 4419; DB 7; Length 822;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSSWIRHGPAMALMGFCMLVGFMRAPACPTSCCKSARICSPSPGIVAPRRP 60  
DB 1 MSSWIRHGPAMALMGFCMLVGFMRAPACPTSCCKSARICSPSPGIVAPRRP 60  
QY 61 NSVDPEITEIFIANQRLIINEDVEAYVGLNLTIVSGLFVFAHKAFLKSNLOHI 120  
DB 61 NSVDPEITEIFIANQRLIINEDVEAYVGLNLTIVSGLFVFAHKAFLKSNLOHI 120  
QY 121 NFRNKLTSLSRKHFRHLDSELLVGNPPTGCDIMWIKTLQBAKSSPTODLYCLNES 180  
DB 121 NFRNKLTSLSRKHFRHLDSELLVGNPPTGCDIMWIKTLQBAKSSPTODLYCLNES 180  
QY 181 SKNIPLANLIQIPNGCLPSANLAAPNLTVBERGSTTSCSVAGDVPVPMYDVGNLVSGHM 240  
DB 181 SKNIPLANLIQIPNGCLPSANLAAPNLTVBERGSTTSCSVAGDVPVPMYDVGNLVSGHM 240  
QY 241 NETSHTQSLRTITNISSDSDGKQISCVAEMLVGEDSDSVNLTVFAPTITPLESPSTDH 300  
DB 241 NETSHTQSLRTITNISSDSDGKQISCVAEMLVGEDSDSVNLTVFAPTITPLESPSTDH 300  
QY 301 WCIPFTVKNPKPALQWFYNGALINESKYICTKHVTNHEHYGCLQDNPTNANGDYT 360  
DB 301 WCIPFTVKNPKPALQWFYNGALINESKYICTKHVTNHEHYGCLQDNPTNANGDYT 360  
QY 361 LIANNEYGKQKQISAFPMGPGIDGAPNYPVYIYEDYTAANDIGDTNRSNETPST 420  
DB 361 LIANNEYGKQKQISAFPMGPGIDGAPNYPVYIYEDYTAANDIGDTNRSNETPST 420  
QY 421 DVIDKTRERHLSVYAVVIVASVGFCLVNLFLIKLARHSFGKGPASVISNDDDSASP 480  
DB 421 DVIDKTRERHLSVYAVVIVASVGFCLVNLFLIKLARHSFGKGPASVISNDDDSASP 480  
QY 481 LHHISNGSNTPSSEGGPDVAITIGMTKIPVLENPQYEGITNSQAKPTFVQHIRHNVL 540  
DB 481 LHHISNGSNTPSSEGGPDVAITIGMTKIPVLENPQYEGITNSQAKPTFVQHIRHNVL 540  
QY 541 KREIGEGAFGKVFIAECYNLCPEQDKILVAVKTLKSDASDARKDPFHEAEELTNLOHEHI 600  
DB 541 KREIGEGAFGKVFIAECYNLCPEQDKILVAVKTLKSDASDARKDPFHEAEELTNLOHEHI 600  
QY 601 VKFYGVCVEGDDPLIMVEFMKGGDLNKLRAHGDAVLMAGNPTELTOGMLHIAQOI 660  
DB 601 VKFYGVCVEGDDPLIMVEFMKGGDLNKLRAHGDAVLMAGNPTELTOGMLHIAQOI 660  
QY 661 AAGWVYLASQHFVARDLATRNCVAGNLVKGDPGSRDVSSTDYIRVGHNTLPIRM 720  
DB 661 AAGWVYLASQHFVARDLATRNCVAGNLVKGDPGSRDVSSTDYIRVGHNTLPIRM 720  
QY 721 PPESIMYRKFTTESDVSLSGVLMIEFTYQKOPYQLSNNEVICITQGRVLOPRTPCQ 780  
DB 721 PPESIMYRKFTTESDVSLSGVLMIEFTYQKOPYQLSNNEVICITQGRVLOPRTPCQ 780  
QY 781 EYVELMLGCMQREBPMKNIKIGHTLLQNLAKASPVYLDILG 822  
DB 781 EYVELMLGCMQREBPMKNIKIGHTLLQNLAKASPVYLDILG 822  
RESULT 10  
ID ADN39974 standard; protein; 822 AA.  
XX  
AC ADN39974;  
XX  
DT 02-DEC-2004 (first entry)

```

XX Neurotrophic tyrosine kinase receptor type 2.
XX
XX cyostatic; gene therapy; human;
XX branching morphogenesis modulating agent; MBM agent.
XX
XX Homo sapiens.
XX
XX MO2004037990-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033549.
XX
XX 23-OCT-2002; 2002US-0420554P.
XX
XX 30-DEC-2002; 2002US-0436941P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Plowman GD, Karim FD, Swimmer C, Habeck HA, Koblipek TI;
XX Schulte-Werker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
XX Odenthal JH, Scheel JK, Will TT, Jin Y, Berke LM, Hai B;
XX Adamkewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
XX Nicoll M;
XX
XX WPI, 2004-365506/34.
XX
XX N-PSDB; ADS92943.
XX
XX Identifying a candidate branching morphogenesis modulating agent for
XX treating cancer comprises contacting the assay system comprising a MBM
XX polypeptide or nucleic acid with a test agent and detecting a test agent-
XX biased activity.
XX
XX Example 3; SEQ ID NO 45; 179pp; English.
XX
XX The invention describes a method of identifying a candidate branching
XX morphogenesis modulating (MBM) agent. The method comprises: providing an
XX assay system comprising a MBM polypeptide or nucleic acid; contacting the
XX assay system with a test agent under conditions where the system provides
XX a reference activity, except for the presence of the test agent; and
XX detecting a test agent-biased activity of the assay system, where a
XX difference between the test agent-biased activity and the reference
XX activity identifies the test agent as a candidate branching morphogenesis
XX modulating agent. Also described are: a method of modulating branching
XX morphogenesis in a mammalian cell; and a method for diagnosing a disease
XX in a patient. The method is useful in identifying a candidate branching
XX morphogenesis modulating agent for preparing a composition for diagnosing
XX or treating cancer. This is the amino acid sequence of a human branching
XX morphogenesis modulating (MBM) protein.
XX
XX Sequence 822 AA;
XX
XX Query Match 100.0%; Score 4419; DB 8; Length 822;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MSSNIRHMGPMARLWGFVGFWRAPACPTSCCKSARINCSPSPGIVAFPRLEP 60
XX |
XX 1 MSSNIRHMGPMARLWGFVGFWRAPACPTSCCKSARINCSPSPGIVAFPRLEP 60
XX |
XX 1 MSSNIRHMGPMARLWGFVGFWRAPACPTSCCKSARINCSPSPGIVAFPRLEP 60
XX |
XX 61 NSVDPENITTEFFINOKRLEIINBDVYAVYGLRNLITVDSGLKFAVHAKFLKNSNLOHI 120
XX |
XX 61 NSVDPENITTEFFINOKRLEIINBDVYAVYGLRNLITVDSGLKFAVHAKFLKNSNLOHI 120
XX |
XX 61 NSVDPENITTEFFINOKRLEIINBDVYAVYGLRNLITVDSGLKFAVHAKFLKNSNLOHI 120
XX |
XX 121 NPTNKLTSLSRKPRHLDSELLVGNPFTCSODIMWIKTLORAKSPDQDLYCLNES 180
XX |
XX 121 NPTNKLTSLSRKPRHLDSELLVGNPFTCSODIMWIKTLORAKSPDQDLYCLNES 180
XX |
XX 121 NPTNKLTSLSRKPRHLDSELLVGNPFTCSODIMWIKTLORAKSPDQDLYCLNES 180
XX |
XX 181 SKNIPLANLQIPNCGLPSEANLAAPNLTVESKSTILSCSVAGDPVPMYMDVGNLVSKM 240
XX |
XX 181 SKNIPLANLQIPNCGLPSEANLAAPNLTVESKSTILSCSVAGDPVPMYMDVGNLVSKM 240
XX |
XX 181 SKNIPLANLQIPNCGLPSEANLAAPNLTVESKSTILSCSVAGDPVPMYMDVGNLVSKM 240
XX |
XX 241 NETSHTQSLRITNISDDSGKOISCVAEMLVGEDQDSVNLTVHAPPTITFLSPSTDH 300
XX

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Db 241 NETSHTQSLRITNISDDSGKOISCVAEMLVGEDQDSVNLTVHAPPTITFLSPSTDH 300
|
Qy 301 WCIPTVYKGNPKPALQWYNGAILNBSKYICTKHVTNHTHYGCIQLDPHTMNNNGDYT 360
|
Db 301 WCIPTVYKGNPKPALQWYNGAILNBSKYICTKHVTNHTHYGCIQLDPHTMNNNGDYT 360
|
Qy 361 LIAKNEYGDEKQISAHFMWPGIDGAPNPNYEDVYEDYGTANDIGDTTNSNEIPST 420
|
Db 361 LIAKNEYGDEKQISAHFMWPGIDGAPNPNYEDVYEDYGTANDIGDTTNSNEIPST 420
|
Qy 421 DVTDKTGREHLSTYAAVVVIVASVVGFCLLVMLFLTKLARSHKFGMKGPASVYSNDDDSASP 480
|
Db 421 DVTDKTGREHLSTYAAVVVIVASVVGFCLLVMLFLTKLARSHKFGMKGPASVYSNDDDSASP 480
|
Qy 481 LHHISNGSNTSSSEGGPDVAVIIGMTKIPYIENPOYFGITNSQLKPDTPVOHIKRANIVL 540
|
Db 481 LHHISNGSNTSSSEGGPDVAVIIGMTKIPYIENPOYFGITNSQLKPDTPVOHIKRANIVL 540
|
Qy 541 KRELGSAGFGKVLAECTYNLCPEODKILVAVKTLKASDPAKODFHRBAELTNLOHEHI 600
|
Db 541 KRELGSAGFGKVLAECTYNLCPEODKILVAVKTLKASDPAKODFHRBAELTNLOHEHI 600
|
Qy 601 VKFYGVCEBDDPLIMVEYMKHGDNLNFKLRAHGPDAVLAEGNPTELTQSOMLHIAQOI 660
|
Db 601 VKFYGVCEBDDPLIMVEYMKHGDNLNFKLRAHGPDAVLAEGNPTELTQSOMLHIAQOI 660
|
Qy 661 AAGVYLASQHFYHRDLATNCLVGENLVKIGDPGMSRDVYSTDYRVGHTMLPIRM 720
|
Db 661 AAGVYLASQHFYHRDLATNCLVGENLVKIGDPGMSRDVYSTDYRVGHTMLPIRM 720
|
Qy 721 PPSIMYRKRTTSDVWSLGVVMEITTYGKQWYQLSNNEVEICTYQGVLYLQRPRTCPQ 780
|
Db 721 PPSIMYRKRTTSDVWSLGVVMEITTYGKQWYQLSNNEVEICTYQGVLYLQRPRTCPQ 780
|
Qy 781 EYVELMIGCQREBPHMKNIKGIHTLLQNLAKSPVYLDILG 822
|
Db 781 EYVELMIGCQREBPHMKNIKGIHTLLQNLAKSPVYLDILG 822
|
RESULT 11
ABUS6699
ID ABUS6699 standard; protein; 838 AA.
XX
XX ABUS6699;
XX
XX 02-Apr-2003 (first entry)
XX
XX Lung cancer-associated polypeptide #292.
XX
XX Lung cancer-associated polypeptide; cyostatic; emphysema;
XX antiinflammatory; anelastic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX unidentified.
XX
XX MO200286443-A2.
XX
XX 31-OCT-2002.
XX
XX 18-Apr-2002; 2002WO-US012476.
XX
XX 18-Apr-2001; 2001US-0284770P.
XX
XX 10-May-2001; 2001US-0290492P.
XX
XX 09-Nov-2001; 2001US-0339245P.
XX
XX 13-Nov-2001; 2001US-0350666P.
XX
XX 29-Nov-2001; 2001US-0334370P.
XX
XX 12-Apr-2002; 2002US-0372246P.
XX
XX (BOSB-) BOS BIOTECHNOLOGY INC.
XX

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PI Aziz N, Murray R;  
 XX WPI; 2003-093161/08.  
 DR N-PSDB; ABX76428.  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX  
 PS Claim 27; Page 418-419; 453pp; English.  
 XX  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridises  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the  
 CC invention  
 XX  
 SQ Sequence 838 AA;  
 XX  
 Query Match 99.6%; Score 4401; DB 6; Length 838;  
 Best Local Similarity 98.1%; Pred. No. 0;  
 Matches 822; Conservative 0; Mismatches 0; Indels 16; Gaps 1;  
 QY 1 MSSWIRHNGPMAMLMGFCMLVGFMRAPFCPTSCKCSARICSPSPGIVAFPRLEP 60  
 DB 1 MSSWIRHNGPMAMLMGFCMLVGFMRAPFCPTSCKCSARICSPSPGIVAFPRLEP 60  
 QY 61 NSVDPENITTEIFIANOKRLIEIINEDVEAYVGLNLTIVDSGLKFAVHAKAFKLSNLOHI 120  
 DB 61 NSVDPENITTEIFIANOKRLIEIINEDVEAYVGLNLTIVDSGLKFAVHAKAFKLSNLOHI 120  
 QY 121 NFRNKLTSLSRKFRHLDSELIIVGNPFTSCSDIMWIKTLQEAASSPTODLYCLNES 180  
 DB 121 NFRNKLTSLSRKFRHLDSELIIVGNPFTSCSDIMWIKTLQEAASSPTODLYCLNES 180  
 QY 181 SKNIPLANLOIPNGGLPSANLAAPULYVEBKSTITSCSVAGDPVPMYVGVNLYVKM 240  
 DB 181 SKNIPLANLOIPNGGLPSANLAAPULYVEBKSTITSCSVAGDPVPMYVGVNLYVKM 240  
 QY 241 NETSHTOGSLRITNISDDSGKOISVAENLVGEDSDSVNLTFAPAPITPLESPBTBHH 300  
 DB 241 NETSHTOGSLRITNISDDSGKOISVAENLVGEDSDSVNLTFAPAPITPLESPBTBHH 300  
 QY 301 WCIPFTYKGNPKPALQWPFYNGAILNESKYICTKIHTNHTYHGCLOLDNPTNANGDYT 360  
 DB 301 WCIPFTYKGNPKPALQWPFYNGAILNESKYICTKIHTNHTYHGCLOLDNPTNANGDYT 360  
 QY 361 LIANKEVGKDEKQISAFHFWGPIDDGANPNYPVITYEDYGTANDIGDTTNRSENPST 420  
 DB 361 LIANKEVGKDEKQISAFHFWGPIDDGANPNYPVITYEDYGTANDIGDTTNRSENPST 420  
 QY 421 DVTDKTGRHLVAVVVIASVGFCLLVMLFLKLARSHKFGMK----- 465  
 DB 421 DVTDKTGRHLVAVVVIASVGFCLLVMLFLKLARSHKFGMKDSWFGFKVKSROG 480  
 QY 466 -GPASVISNDDDSAPLHHISNGSNTBSSSGGPDVAVIIGTKIPIVLENPOYFGITNSQL 524  
 DB 466 -GPASVISNDDDSAPLHHISNGSNTBSSSGGPDVAVIIGTKIPIVLENPOYFGITNSQL 524  
 QY 481 VGPASVISNDDDSAPLHHISNGSNTBSSSGGPDVAVIIGTKIPIVLENPOYFGITNSQL 540  
 DB 481 VGPASVISNDDDSAPLHHISNGSNTBSSSGGPDVAVIIGTKIPIVLENPOYFGITNSQL 540

QY 525 KPDTFVOHKKRNIIVLKRLEBEGAFGKVFIAECYNI.CPEODKILVAVKTLKASDNARKD 584  
 DB 541 KPDTFVOHKKRNIIVLKRLEBEGAFGKVFIAECYNI.CPEODKILVAVKTLKASDNARKD 600  
 QY 585 FHRBAELLTLQDHEHYKFPYGVCEGDPILIMVBYMKHGDLNFKLRAHGDAVIMAGNP 644  
 DB 601 FHRBAELLTLQDHEHYKFPYGVCEGDPILIMVBYMKHGDLNFKLRAHGDAVIMAGNP 660  
 QY 645 PTELTSQMLHIQOQLAGNVYLASQHFVHRDLATRNCLVGENLIVIGDFGMSRDVYST 704  
 DB 661 PTELTSQMLHIQOQLAGNVYLASQHFVHRDLATRNCLVGENLIVIGDFGMSRDVYST 720  
 QY 705 DYRVGSHMLPIRMMPRESIMYRKFTTESDWSLGVLMIEFTYQKQPYQLSNNEVIE 764  
 DB 721 DYRVGSHMLPIRMMPRESIMYRKFTTESDWSLGVLMIEFTYQKQPYQLSNNEVIE 780  
 QY 765 CITQGRVLQRPRTCPQEVYELMLGCWQREPMKRNKIGITLLONLAKASPVYLDIIG 822  
 DB 781 CITQGRVLQRPRTCPQEVYELMLGCWQREPMKRNKIGITLLONLAKASPVYLDIIG 838  
 RESULT 12  
 ADN39078  
 ID ADN39078 standard; protein; 838 AA.  
 XX  
 AC ADN39078;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:396.  
 XX  
 KW Human: differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; autoimmune disease;  
 KW inflammatory disease; autoimmune disease;  
 KW rectinal neovascularisation syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
 KW vulnereary; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 PN WO2003042661-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PE 13-NOV-2002; 2002WC-US036810.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334383P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-035250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368809P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 05-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (BOSB-) BOS BIOTECHNOLOGY INC.  
 XX  
 PI Afer D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA,  
 XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
 DR WPI; 2003-468649/44.









Db	540	KRELGEAFGKVFPLABECYNLCPEODKILVAVKTLKDASDNARKDFHREAEILLTNLOHEHI	599
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Db	600	VKPYGVCEBGPPLIMVFEMGHGDLNKEFLRAHGPDAVIMAEGNPPTTELTOSONLHIAQOI	659
Qy	661	AAGNVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYRVGHTMLPIRM	720
Db	660	AAGNVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYRVGHTMLPIRM	719
Qy	721	PPESIMYRKFTTESDVWSLGIVLWEIFTYKQOPWYQLSNNEVIBCTTQGRVLORRPTCPQ	780
Db	720	PPESIMYRKFTTESDVWSLGIVLWEIFTYKQOPWYQLSNNEVIBCTTQGRVLORRPTCPQ	779
Qy	781	EVEIEMLGQWOREBPHMRKNIGIHITLQNLAKASPVYIDLIG	822
Db	780	EVEIEMLGQWOREBPHMRKNIGIHITLQNLAKASPVYIDLIG	821

Search completed: February 17, 2005, 00:24:24  
 Job time : 174 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 17, 2005, 00:10:23 ; Search time 178 Seconds  
(without alignments)  
2364.770 Million cell updates/sec

Title: US-10-645-546-2  
Perfect score: 4419  
Sequence: 1 MSSMIRWHPMARLMGFCW.....IHTLLQNIKASPYVLDILG 822

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4419	100.0	822	1 TRKB_HUMAN	Q16620 homo sapien
2	4401	99.6	838	2 O8WKJ7	O8WKJ7 homo sapien
3	4179.5	94.6	821	1 TRKB_MOUSE	P15209 mus musculu
4	4162.5	94.2	821	1 TRKB_RAT	O63604 rattus norv
5	3426	77.5	818	1 TRKB_CHICK	Q91987 gallus gall
6	3091.5	70.0	821	2 O9YH44	O9YH44 xenopus lae
7	3078.5	69.7	811	2 O9YH43	O9YH43 xenopus lae
8	2896.5	65.5	669	2 O6B515	O6B515 poephila gu
9	2826	64.0	553	2 O8WKJ5	O8WKJ5 homo sapien
10	2296	52.0	825	2 O6VNS1	O6VNS1 mus musculu
11	2282.5	51.9	476	2 O8OWU0	O8OWU0 mus musculu
12	2277	51.5	839	1 TRKB_HUMAN	Q16288 homo sapien
13	2277	51.5	839	2 O75682	O75682 homo sapien
14	2275	51.5	827	1 TRKB_CHICK	O91044 gallus gall
15	2266.5	51.3	864	1 TRKB_RAT	O03351 rattus norv
16	2178	49.3	825	1 TRKB_PIG	P24786 sus scrofa
17	2107	47.7	486	2 O9PST9	O9PST9 xenopus lae
18	1943.5	44.0	790	2 O90699	O90699 gallus gall
19	1916.5	43.4	778	1 TRKA_CHICK	O91009 gallus gall
20	1901.5	43.0	796	1 TRKA_HUMAN	P04629 homo sapien
21	1901	43.0	799	1 TRKA_RAT	P35739 rattus norv
22	1430.5	32.1	282	2 O91373	O91373 xenopus. tr
23	1263.5	28.6	476	2 O7ZXU8	O7ZXU8 xenopus lae
24	1249	28.3	503	2 O15655	O15655 homo sapien
25	1098.5	24.9	794	1 TRK1_LYMSST	O76997 lymnaea sca
26	991	22.4	612	2 O922P9	O922P9 mus musculu
27	989	22.4	612	2 O96CY4	O96CY4 homo sapien
28	969	21.9	185	2 O9GMA1	O9GMA1 cercopithec
29	858.5	19.4	868	1 MUSK_RAT	O62838 rattus norv
30	854	19.3	869	1 MUSK_HUMAN	O15146 homo sapien
31	850.5	19.2	868	1 MUSK_MOUSE	O61006 mus musculu

32	844.5	19.1	1145	2 O9BK18	O9BK18 alysia cal
33	798	18.1	946	2 O07153	O07153 torpedo cal
34	789.5	17.9	947	1 MUSK_CHICK	O8AXY6 gallus gall
35	763.5	17.3	502	2 O92200	O92200 mus musculu
36	757	17.1	626	2 O7OIP0	O7OIP0 anopheles g
37	749	16.9	685	1 ROR1_DROME	O24488 drosophila
38	736	16.7	553	2 O7Z2S2	O7Z2S2 brachydanio
39	734	16.6	354	2 O9DDA2	O9DDA2 xenopus lae
40	731	16.5	863	2 O7Q5T3	O7Q5T3 anopheles g
41	722	16.3	937	1 ROR1_HUMAN	O01973 homo sapien
42	720	16.3	896	2 O705C2	O705C2 gallus gall
43	717.5	16.2	724	1 ROR2_DROME	O9V6K3 drosophila
44	716	16.2	178	2 O95K65	O95K65 macaca fasc
45	716	16.2	948	2 O9Y1Y6	O9Y1Y6 ephydactia f

## ALIGNMENTS

RESULT 1  
ID: TRKB\_HUMAN STANDARD; PRT; 822 AA.  
AC Q16620; Q16675; O8WKJ6;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB  
DE tyrosine kinase) (GPI45-TKb) (TK-B).  
GN Name=NTK2; Synonyms=TRKB;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
[1]  
RN SEQUENCE FROM N.A. (ISOFORM TRKB).  
RP TISSUE=Hippocampus;  
RC MEDLINE=95309922; PubMed=7789988;  
RA Nakagawa A., Liu X.-G., Ikegaki N., White P.S., Yamashiro D.J.,  
RA Nyman L.M., Biegel J.A., Brodeur G.M.,  
RT "Cloning and chromosomal localization of the human TRK-B tyrosine  
RT kinase receptor gene (NTK2)."  
RL Genomics 25:538-546 (1995).  
[2]  
RN SEQUENCE FROM N.A. (ISOFORMS TRKB AND TRKB-T1).  
RP TISSUE=Brain;  
RC MEDLINE=95123473; PubMed=7823156;  
RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,  
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.,  
RT "Human trks: molecular cloning, tissue distribution, and expression of  
RT extracellular domain immunoadhesins."  
RL J. Neurosci. 15:477-491 (1995).  
[3]  
RN SEQUENCE FROM N.A. (ISOFORM TRKB-T1).  
RP TISSUE=Hippocampus;  
RC MEDLINE=95022162; PubMed=7936202; DOI=10.1016/0306-4522(94)90507-X;  
RA Allen S.J., Dawbarn D., Eckford S.D., Wilcock G.K., Ashcroft M.,  
RA Colebrook S.M., Feeney R., Macgowan S.H.,  
RT "Cloning of a non-catalytic form of human trkb and distribution of  
RT messenger RNA for trkb in human brain."  
RL Neuroscience 60:825-834 (1994).  
[4]  
RN SEQUENCE FROM N.A. (ISOFORMS TRKB; TRKB-T1 AND TRKB-T-SHC).  
RP MEDLINE=91656983; PubMed=11798189; DOI=10.1006/dbpc.2001.6301;  
RA Stoklov P., Caetren E., Stamm S.,  
RT "Analysis of the human trkb gene genomic organization reveals novel  
RT trkb isoforms, unusual gene length, and splicing mechanism."  
RL Biochem. Biophys. Res. Commun. 290:1054-1065 (2002).  
[5]  
RN SEQUENCE FROM N.A. (ISOFORM TRKB-T1), AND VARIANT ARG-309.  
RP Steinbeck J.A., Thomsen S., Messig U., Leyboldt F., Leverenz J.,  
RA Wehner A.,  
RT "Full length truncated trkb sequence identified in a screen for genes  
RT regulated by ischemic preconditioning.";

Submitted (May-2002) to the EMBL/GenBank/DBJ databases.

[6] SEQUENCE FROM N.A. (ISOFORM TRKB-T1).

CC TISSUE=Brain;

CC MEDLINE=22289857; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strassberg R.L., Felingold E.A., Gronow L.H., Derge J.G.,

RA Kleinsch R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buecok K.H., Schenker C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,

RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stancione M., Soares M.B., Bonaldi M.F., Cavaletti T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carantini P., Prange S.J.,

RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Boeck S.A., McKean P.J., McKernan K.V., Malek J.A., Gunatratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,

RA Whiting R.W., Madan A.C., Shewchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butcherfield Y.S., Krzyzinski M.I., Skalska U., Smallus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [7]

RP DISULFIDE BONDS.

RP MEDLINE=96004804; PubMed=7574684; DOI=10.1006/abbi.1995.1460;

RA Hanlu M., Talemehmo J., Le Q., Katta V., Melcher A., Rohde M.F.,

RT "Extracellular domain of neurotrophin receptor trkB: disulfide

RT structure, N-glycosylation sites, and ligand binding.";

RL Arch. Biochem. Biophys. 322:255-264(1995).

CC -1- FUNCTION: Receptor for brain-derived neurotrophic factor (BDNF),

CC neurotrophin-3 and neurotrophin-4/5 but not nerve growth factor

CC (NGF). Involved in the development and/or maintenance of the

CC nervous system. This is a tyrosine-protein kinase receptor. Known

CC substrates for the TRK receptors are Shc1, PI-3 kinase, and PLC-

CC gamma-1.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.

CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low

CC affinity) and dimeric (high affinity) structures (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Comment=Additional isoforms seem to exist;

CC Name=TrkB;

CC IsoId=Q16620-1; Sequence=Displayed;

CC Name=TrkB-T1;

CC IsoId=Q16620-2; Sequence=VSP\_002901, VSP\_002902;

CC Name=TrkB-T-Shc;

CC IsoId=Q16620-3; Sequence=VSP\_002903, VSP\_002904;

CC -1- TISSUE SPECIFICITY: Isoform TrkB is widely expressed, mainly in

CC the nervous tissue.

CC In the CNS, expression is observed in the

CC cerebral cortex, hippocampus, thalamus, choroid plexus, granular

CC layer of the cerebellum, brain stem, and spinal cord. In the

CC peripheral nervous system, it is expressed in many cranial

CC ganglia, the ophthalmic nerve, the vestibular system, multiple

CC facial structures, the submaxillary glands, and dorsal root

CC ganglia. Isoform TrkB-T1 is expressed in multiple tissues, mainly

CC in brain, pancreas, kidney and heart. Isoform TrkB-T-Shc is

CC predominantly expressed in brain.

CC -1- PTM: Ligand-mediated auto-phosphorylation.

CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin

CC receptor subfamily.

CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC modified and this statement is not removed. Usage by and for commercial

CC	entities require a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .		
CC	-----		
DR	EMBL, U12140, AAC51371.1, -		
DR	EMBL, S76473, AAB33109.1, -		
DR	EMBL, S76474, AAB33110.1, -		
DR	EMBL, X75958, CAA53571.1, -		
DR	EMBL, AF410900, AAL67966.1, -		
DR	EMBL, AF508964, AAM7876.1, -		
DR	EMBL, BC031835, AAB1835.1, -		
DR	PIR, A56853, A56853.		
DR	PIR, I73631, I73631.		
DR	PDB, 1HCF, X-ray, X/Y=283-383.		
DR	PDB, 1WMB, X-ray, X=283-385.		
DR	Genew, HGNC:8032, NTRK2.		
DR	H-InvdB, HIX0008134, -		
DR	MIM, 600456, -		
DR	GO, GO:0005887, C:integral to plasma membrane; TAS.		
DR	GO, GO:0005015, P:neurotrophin TRKB receptor activity; TAS.		
DR	GO, GO:0007169, P:transmembrane receptor protein tyrosine kin. ., TAS.		
DR	InterPro, IPR007110, Ig-like.		
DR	InterPro, IPR011009, Kinase like.		
DR	InterPro, IPR000372, LRR_Nterm.		
DR	InterPro, IPR000719, Prot_kinase.		
DR	InterPro, IPR002011, ReceptCytKinsII.		
DR	InterPro, IPR001245, Tyr_kinase.		
DR	InterPro, IPR008266, Tyr_kinase_AS.		
DR	Pfam, PF01462, LRRNT. 1.		
DR	Pfam, PF00069, Pkinase. 1.		
DR	PIRINTS, PR00109, TYRKINASE.		
DR	PRODOM, PD000001, Prot_kinase. 1.		
DR	PROSITE, PS50835, Ig_Like. 1.		
DR	PROSITE, PS00107, PROTEIN_KINASE_ATP. 1.		
DR	PROSITE, PS50011, PROTEIN_KINASE_DOM. 1.		
DR	PROSITE, PS00109, PROTEIN_KINASE_TYR. 1.		
DR	PROSITE, PS00233, RECEPTOR_TYR_KIN_11. 1.		
KM	3D-structure; Alternative splicing; ATP-binding; Glycoprotein;		
KM	Immunoglobulin domain; Leucine-rich repeat; Neurogenesis;		
KW	Phosphorylation; Polymorphism; Receptor; Repeat; Signal; Transferase;		
KW	Transmembrane; Tyrosine-protein kinase.		
FT	SIGNAL	1	31
FT	CHAIN	32	822
FT	DOMAIN	32	430
FT	TRANSMEM	431	454
FT	DOMAIN	455	822
FT	REPEAT	72	93
FT	REPEAT	96	117
FT	DOMAIN	197	282
FT	DOMAIN	295	365
FT	DOMAIN	538	807
FT	NP_BIND	544	552
FT	BINDING	572	572
FT	ACT_SITE	676	676
FT	DISULFID	32	38
FT	DISULFID	36	45
FT	DISULFID	152	176
FT	DISULFID	154	194
FT	DISULFID	218	266
FT	DISULFID	302	345
FT	MOD_RES	516	516
FT	MOD_RES	702	702
FT	MOD_RES	706	706
FT	MOD_RES	707	707
FT	MOD_RES	817	817
FT	SITE	516	516
FT	SITE	817	817
FT	similarity).		



FT CARBOHD 67 67 N-linked (GlcNAc. . .) (Potential) .  
 FT CARBOHD 95 95 N-linked (GlcNAc. . .) (Potential) .  
 Query Match 100.0%; Score 4419; DB 1; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 4,4e-251;  
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRMHGPMARMLMGFCMLVGFWRRAAFACPTSCCKSASRIWCSDPSPGIVAFLPRLEP 60  
 DB 1 MSSWIRMHGPMARMLMGFCMLVGFWRRAAFACPTSCCKSASRIWCSDPSPGIVAFLPRLEP 60  
 QY 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLQHI 120  
 DB 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLQHI 120  
 QY 121 NPTNKLTSLSRKPRHLDISELLVGNPFTCSQDIIWIKTLQKAKSSPDQDLYCLNES 180  
 DB 121 NPTNKLTSLSRKPRHLDISELLVGNPFTCSQDIIWIKTLQKAKSSPDQDLYCLNES 180  
 QY 181 SKNIPLANLOIPNCGLP SANLAAPNLVTEBKSITLSCSVAQDPVPMNYMDVGNLVSKM 240  
 DB 181 SKNIPLANLOIPNCGLP SANLAAPNLVTEBKSITLSCSVAQDPVPMNYMDVGNLVSKM 240  
 QY 241 NETSHTQSLRITNISDDSGKQISCVAEINVGEDQSVNLTVHFAPTITFLSPSDH 300  
 DB 241 NETSHTQSLRITNISDDSGKQISCVAEINVGEDQSVNLTVHFAPTITFLSPSDH 300  
 QY 301 WCIPFTYKGNPKPALQWRYNAGAILNESKTYCTKHVTNHTHYHGLQDNDPTHANNNGDYT 360  
 DB 301 WCIPFTYKGNPKPALQWRYNAGAILNESKTYCTKHVTNHTHYHGLQDNDPTHANNNGDYT 360  
 QY 361 LIAKNEYGKDEKQISAHFMGWPIDGDPANPNVPIYEDYGTAAANDIGDTTNRSEIPIST 420  
 DB 361 LIAKNEYGKDEKQISAHFMGWPIDGDPANPNVPIYEDYGTAAANDIGDTTNRSEIPIST 420  
 QY 421 DVTDKTGRHLVYAVVVIASVGECLLWMLFLKLARHSKFGMKGPASVISNDDSNASP 480  
 DB 421 DVTDKTGRHLVYAVVVIASVGECLLWMLFLKLARHSKFGMKGPASVISNDDSNASP 480  
 QY 481 LHHISNGSTSSSSSGGPDVAITIGMTKPIVENPQYSEITNSQLKPDVFQHIKRNHIVL 540  
 DB 481 LHHISNGSTSSSSSGGPDVAITIGMTKPIVENPQYSEITNSQLKPDVFQHIKRNHIVL 540  
 QY 541 KREIAGEBAGFYFLAECYNLCPEODKILVAVTLDASDANKDPHREABLLTNLOHEHI 600  
 DB 541 KREIAGEBAGFYFLAECYNLCPEODKILVAVTLDASDANKDPHREABLLTNLOHEHI 600  
 QY 601 VKFYGVCEGDPPLIMVFPEYMGHGLDKFLRAHGPDAVLAEGNPTELTOGOMLHIAQOI 660  
 DB 601 VKFYGVCEGDPPLIMVFPEYMGHGLDKFLRAHGPDAVLAEGNPTELTOGOMLHIAQOI 660  
 QY 661 AAGMYVILASQHFVRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYVGVGHMLPIRMW 720  
 DB 661 AAGMYVILASQHFVRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYVGVGHMLPIRMW 720  
 QY 721 PPESTMYKFTTESVMSLGVLMELFTYGKOPWQUSNNVEITECTITGGRVLAQRPRTCPQ 780  
 DB 721 PPESTMYKFTTESVMSLGVLMELFTYGKOPWQUSNNVEITECTITGGRVLAQRPRTCPQ 780  
 QY 781 EYVELMLGCMQREPHMRKIKGIHTLONLAKASPVYDIILG 822  
 DB 781 EYVELMLGCMQREPHMRKIKGIHTLONLAKASPVYDIILG 822

RESULT 2  
 Q8WKJ7 PRELIMINARY; PRT; 838 AA.  
 AC Q8WKJ7;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Neurotrophin receptor tyrosine kinase type 2.  
 GN Name=NTRK2;

OS Homo sapiens (Human) .  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=21656983; Pubmed=11798182;  
 RA Stoolov P., Castrén E., Stamm S.;  
 RT "Analysis of the human trkB gene genomic organization reveals novel  
 trkB isoforms, unusual gene length, and splicing mechanism.";  
 RL Biochem. Biophys. Res. Commun. 290:1054-1065(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Stoolov P.G., Castrén E., Stamm S.;  
 RA Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin  
 CC receptor subfamily.  
 DR EMBL; AF410899; AAL67965.1; -.  
 DR HSSP; O16620; 1MBW.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0005524; F: ATP binding; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0016740; F: transferase activity; IEA.  
 DR GO; GO:0004714; F: transmembrane receptor protein tyrosine kin. . .; IEA.  
 DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.  
 DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; IEA.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot. kinase; 1.  
 DR SMART; SM00408; IGC2; 1.  
 DR SMART; SM00082; LRCT; 1.  
 DR SMART; SM00013; LRNT; 1.  
 DR SMART; SM00219; TYKC; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS0107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR TYR\_KIN\_II; 1.  
 DR ATP-binding; kinase; phosphorylation; Receptor; Transferase;  
 KW transmembrane; tyrosine-protein kinase.  
 SQ SEQUENCE 838 AA; 93825 MW; 130C95A9D895432 CRC64;

Query Match 99.6%; Score 4401; DB 2; Length 838;  
 Best Local Similarity 96.1%; Pred. No. 5.1e-250;  
 Matches 822; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

QY 1 MSSWIRMHGPMARMLMGFCMLVGFWRRAAFACPTSCCKSASRIWCSDPSPGIVAFLPRLEP 60  
 DB 1 MSSWIRMHGPMARMLMGFCMLVGFWRRAAFACPTSCCKSASRIWCSDPSPGIVAFLPRLEP 60  
 QY 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLQHI 120  
 DB 61 NSVDPENITTEIFIANOKRLEIINEDDVEAYVGLRNLTIVDSGLKFAVAKAFKNSNLQHI 120  
 QY 121 NPTNKLTSLSRKPRHLDISELLVGNPFTCSQDIIWIKTLQKAKSSPDQDLYCLNES 180  
 DB 121 NPTNKLTSLSRKPRHLDISELLVGNPFTCSQDIIWIKTLQKAKSSPDQDLYCLNES 180  
 QY 181 SKNIPLANLOIPNCGLP SANLAAPNLVTEBKSITLSCSVAQDPVPMNYMDVGNLVSKM 240  
 DB 181 SKNIPLANLOIPNCGLP SANLAAPNLVTEBKSITLSCSVAQDPVPMNYMDVGNLVSKM 240  
 QY 241 NETSHTQSLRITNISDDSGKQISCVAEINVGEDQSVNLTVHFAPTITFLSPSDH 300  
 DB 241 NETSHTQSLRITNISDDSGKQISCVAEINVGEDQSVNLTVHFAPTITFLSPSDH 300  
 QY 301 WCIPFTYKGNPKPALQWRYNAGAILNESKTYCTKHVTNHTHYHGLQDNDPTHANNNGDYT 360  
 DB 301 WCIPFTYKGNPKPALQWRYNAGAILNESKTYCTKHVTNHTHYHGLQDNDPTHANNNGDYT 360  
 QY 361 LIAKNEYGKDEKQISAHFMGWPIDGDPANPNVPIYEDYGTAAANDIGDTTNRSEIPIST 420

Db 361 LIANKGKQKBEKQSAHFMGHPGDDANPNYVIEDYGTANDGDTTNSNEIPST 420  
 Qy 421 DVTDKTGREHLSVYAVVAVVAVSVGFCILVLMFLKAKARSHKSPGKK----- 465  
 Db 421 DVTDKTGREHLSVYAVVAVVAVSVGFCILVLMFLKAKARSHKSPGKKDSWFGFKVKSROG 480  
 Qy 466 -GPRSVISNDDSDASPLHHISNGSNTSSSGEGPDANIIGMTKIPVIENTPOYFQITNSOL 524  
 Db 481 VGPASVISNDDSDASPLHHISNGSNTSSSGEGPDANIIGMTKIPVIENTPOYFQITNSOL 540  
 Qy 525 KPDPFYOHKRNHVLKREIGEGAFKGYFLABECNCLPEODKILVAKTLKXASDNARKD 584  
 Db 541 KPDPFYOHKRNHVLKREIGEGAFKGYFLABECNCLPEODKILVAKTLKXASDNARKD 600  
 Qy 585 FHREAEELITLQHEHIVKFGVGVCEGDPDLINVEFYMKHGLDKELRAHGPDAVLAEGNP 644  
 Db 601 FHREAEELITLQHEHIVKFGVGVCEGDPDLINVEFYMKHGLDKELRAHGPDAVLAEGNP 660  
 Qy 645 PTELTGQMLHIAQOIAAGVYTLASQHFVHRDLATNCLVGENILVTKIGDFGMSRDVYST 704  
 Db 661 PTELTGQMLHIAQOIAAGVYTLASQHFVHRDLATNCLVGENILVTKIGDFGMSRDVYST 720  
 Qy 705 DYRVGSHHTMLPIRMPEPESIMRKFTTESDVSLSGVLMETFYGKOPWYQSLNNEVIE 764  
 Db 721 DYRVGSHHTMLPIRMPEPESIMRKFTTESDVSLSGVLMETFYGKOPWYQSLNNEVIE 780  
 Qy 765 CITGGRVLOBPRTCPQEVYELMLGCMQREPRMRKNIKGIHTLLONLAKASPVYLDILG 822  
 Db 781 CITGGRVLOBPRTCPQEVYELMLGCMQREPRMRKNIKGIHTLLONLAKASPVYLDILG 838

RESULT 3  
 TRKB MOUSE STANDARD; PRT; 821 AA.

ID TRKB MOUSE STANDARD; PRT; 821 AA.  
 AC P15209; O91XJ9;  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB  
 DE tyrosine kinase) (GPI45-TrkB/GP95-TrkB) (TrkB-B).  
 GN Name=Trk2; Synonyms=Trkb;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM GPI45-TRKB).  
 RC TISSUE=Brain;  
 RX MEDLINE=90059970; PubMed=2555172;  
 RA Klein R., Parada L.F., Coulier F., Barbacid M.;  
 RT "trkb, a novel tyrosine protein kinase receptor expressed during mouse  
 RT neural development.";  
 RL EMBO J. 8:3701-3709(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS GPI45-TRKB AND GP95-TRKB).  
 RC TISSUE=Brain;  
 RX MEDLINE=90263089; PubMed=2160854; DOI=10.1016/0092-8674(90)90476-U;  
 RA Klein R., Conway D., Parada L.F., Barbacid M.;  
 RT "The trkb tyrosine protein kinase gene codes for a second neurogenic  
 RT receptor that lacks the catalytic kinase domain.";  
 RL Cell 61:647-656(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM GP95-TRKB).  
 RC STRAIN=ND; TISSUE=Thymus;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakai I., Otsu M., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,  
 RA Baldairell R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirral L.M., Kratnap A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Datta E., Dregant T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Giesel C., Godzik A., Gough J.,  
 RA Grimmond S., Guenichon S., Hirokawa N., Jackson J.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.U.,  
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagasima T., Numata K., Okido T., Paven M.J., Pereira G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reid D.J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Tarekna Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Vardaro R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shirozaki T., Waki K., Waki K., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh N., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yenumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS L1 AND L10).  
 RC TISSUE=Trigeminal ganglion;  
 RX MEDLINE=97294706; PubMed=9148911; DOI=10.1074/jbc.272.20.13019;  
 RA Ninkina N., Grashchuk M., Buchman V.L., Davies A.M.;  
 RT "Trkb variants with deletions in the leucine-rich motifs of the  
 RT extracellular domain.";  
 RL J. Biol. Chem. 272:13019-13025(1997).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=91249395; PubMed=1645620; DOI=10.1016/0092-8674(91)90396-G;  
 RA Soppet D., Escandon E., Maragos J., Middlemas D.S., Reid S.W.,  
 RA Blair J., Burton L.E., Stanton B.R., Kaplan D.R., Hunter T.,  
 RA Nicolls K., Parada L.F.;  
 RT "The neurotrophic factors brain-derived neurotrophic factor and  
 RT neurotrophin-3 are ligands for the trkb tyrosine kinase receptor.";  
 RL Cell 65:895-903(1991).  
 CC -1- FUNCTION: Receptor for brain-derived neurotrophic factor (BDNF),  
 CC neurotrophin-3 and neurotrophin-4/5 but not nerve growth factor  
 CC (NGF). Involved in the development and/or maintenance of the  
 CC nervous system. This is a tyrosine-protein kinase receptor. Known  
 CC substrates for the trkb receptors are SHC1, PI-3 kinase, and PLC-  
 CC gamma-1.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low  
 CC affinity) and dimeric (high affinity) structures.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Comment=Alternative splicing; Named isoforms=4;  
 CC Name=GPI45-TRKB; Synonyms=I3;  
 CC IsoId=GPI5209-1; Sequence=Displayed;  
 CC Name=GP95-TRKB; Synonyms=TI;  
 CC IsoId=GPI5209-2; Sequence=VSP\_002908, VSP\_002909;  
 CC Name=L1;  
 CC IsoId=GPI5209-3; Sequence=VSP\_002907;  
 CC Name=L10;  
 CC IsoId=GPI5209-4; Sequence=VSP\_002905, VSP\_002906;  
 CC -1- TISSUE SPECIFICITY: The different forms are differentially  
 CC expressed in various cell types.  
 CC -1- PTM: Ligand-mediated auto-phosphorylation.  
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin  
 CC receptor subfamily.  
 CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.  
 CC -----  
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FT	CARBOND	67	67	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	95	95	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	121	121	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	178	178	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	205	205	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	241	241	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	254	254	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	280	280	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	325	325	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	338	338	N-linked (GlcNAc . .)	(Potential) .
FT	CARBOND	411	411	N-linked (GlcNAc . .)	(Potential) .
FT	VASAPLIC	71	71	I -> M (in isoform L10).	
FT			/FtId=VSP_002905.		
FT			Missing (in isoform L10).		
FT	VASAPLIC	72	143	FtId=VSP_002906.	
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Query Match            94.6%; Score 4179.5; DB 1; Length 821;					
Beet Local Similarity    93.9%; Pred. No. 5e-237;					
Matches    772; Conservative    27; Mismatches    22; Indels    1; Gaps    1;					
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OY	1	MSSWIRMGPMALMGCFCMLVGFMPMAFAFCAPTSCSKCSASRIWCSDPSPGIIVAFPRLEP	60		
Dd	1	MSPLKMHGPMALMKGCLLVLFQWPAISLACPISCCKSARIKCTESPEIVAFLRLEP	60		
OY	61	NSVDPENITELIFANOKRELIINEDVEAYVGLRNLTITVDSGLKFVAHKAFLKNISNLOHI	120		
Dd	61	NSVDPENITELLIANOKRELIINEDVEAYVGLRNLTITVDSGLKFVAYAKAFLKSNLSLHI	120		
OY	121	NFTNRKLITSLSRKFRHLDELILVGNPFPCSDIMWIKILOEAKSPDPODIYLCLNES	180		
Dd	121	NFTNRKLITSLRRFRRLDSDLILTGPPFCSCDIMWLKLOETKSPDPQODLYCLNES	180		
OY	181	SKNIPLANIOJPNCGLPSPANLAENLTVBECKSTITLSCSVAGDEVPMNYMVGVNLVSCHM	240		
Dd	181	SKNPPLANIOJPNGCLPSARAENLTVBECKSTITLSCSVAGDEPLTLYMVGVNLVSCHM	240		
OY	241	NETSHTOGSRLRTINISSDDSGKOISCVAEMLVGEDODSVNLTVHAPPTITLESPTSDBH	300		
Dd	241	NETSHTOGSRLRTINISSDDSGKOISCVAEMLVGEDODSVNLTVHAPPTITLESPTSDBH	300		
OY	301	WCIPFYTKGNKPALOMFYNGALLNESKYICTKHVNHTHYHGCLOLDNPTHANNGYT	360		
Dd	301	WCIPFYTKGNKPALOMFYNGALLNESXYICTKHVNHTHYHGCLOLDNPTHANNGYT	360		
OY	361	LIAKREYGKOEKOISAHFMGWPIGDGANPVYDVIEVDXTAANDIGDTTRNSAEIPTST	420		
Dd	361	LMAONEGKDEROJSAHFMGRPYVDYETPNYPVLEVLBYDM-TPTPDIGDTTRNKSNLEIPTST	419		
OY	421	DVTXKTGEHLSVYAUVVIASVVFCLLVMLFLKLARKSHFKGMKGPASVISNDSDSASP	480		
Dd	420	DVADQSREHLSVYAUVVIASVVFCLLVMLLLKLARKSHFKGMKGPASVISNDSDSASP	479		
OY	481	LHHISNGSNTPSSSEGGDAVITGMTKI PVIENTPOYFGITNSOLKPDTFVOHIRKHNIVL	540		
Dd	480	LHHISNGSNTPSSSEGGDAVITGMTKIPVIENTPOYFGITNSOLKPDTFVOHIRKHNIVL	539		
OY	541	KREIBGBGFGVFLAECYNLCPEBDKTLIVAKTLKDASDNARKDFHRBAELITLLOHEHI	600		
Dd	540	KREIBGBGFGVFLAECYNLCPEBDKTLIVAKTLKDASDNARKDFHRAELITLLOHEHI	599		
OY	601	VKFPYGVCEGQPLTMVEFEVMHGDLINTFLRAHGDAVLMAEGNPTELTOSQMLHAQQI	660		
Dd	600	VKFPYGVCEGQPLTMVEFEVMHGDLINTFLRAHGDAVLMAEGNPTELTOSQMLHAQQI	659		
OY	661	AAGNVYLASOHFVARIDLATRNCLVGENILVKIGDFGMSRDVYSTDYRVGGHTMLPIRMW	720		
Dd	660	AAGNVYLASOHFVARIDLATRNCLVGENILVKIGDFGMSRDVYSTDYRVGGHTMLPIRMW	719		
OY	721	PRESIMRKFTTESDWSLGVLMIEIFTYGOQPYYOISNNNEVEICIQGVALQRPRTCPQ	780		
Dd	720	PPSIMRKFTTESDWSLGVLMIEIFTYGOQPYYOISNNNEVEICITQGVLRQRPRTCPQ	779		
OY	781	EVEYELMGCMQRBPMMRNKINGITTTLLONLAKAPVYLDILG	822		



FT	VARSPLIC	477	821	/FTID=VSP 002910.	!
FT				Missing (in isoform T1).	
FT	VARSPLIC	466	474	/FTID=VSP_002911.	
FT				PASVISND -> KQCAVFPAS (in isoform T2).	
FT	VARSPLIC	475	821	/FTID=VSP_002912.	
FT				Missing (in isoform T2).	
FT				/FTID=VSP 002913.	
SO	SEQUENCE	821 AA;	92186 MW;	0DDACBA212CDA0E CRC64;	
Query Match					
Best Local Similarity 93.6%; Score 4162.5; DB 1; Length 821;					
Matches 769; Conservative 25; Mismatches 27; Indels 1; Gaps 1					
QY	1	MSSNRHMGPMARMLWGFCMLVGGWRRAAFACPTSCCKGSASIKWSDSPGIVARPRLEP	60		
DB	1	MSPMRHMGPMAARLMGCLLVLGFWRASLACPMSCCKSTTRTWCTEPSPGIVAPPRLEP	60		
QY	61	NSVPEPNTETEIFIANQKRLIINEDDEAVAYGLRYMLTYDSGLKRVAAKAFIKNSLQHI	120		
DB	61	NSIDPENITELIANQKRLIINEDDEAVAYGLKRLTYDSGLKVAAYAKFKNGRLHI	120		
QY	121	NFRNKLTLSRKHFRLDSELIVGNPFTSCDMMIKTLQKAKSPDTOLYCLNES	180		
DB	121	NFTNRKLTLSRRHRRLDSDLITGNPFTSCDMMIKTLQKAKSPDTOLYCLNES	180		
QY	181	SKNIPLANLIQIPNCGLPASNLAAPLTYEBGSKITLSCGSVADPVNMTVDGNIVSKIM	240		
DB	181	SKNIPLANLIQIPNCGLPASNLAAPLTYEBGSKVITISCSVGDPPLTYLWDGNIVSKIM	240		
QY	241	NETSHOTSARITINSSDDSGKQISCVAMENVGEODSNTLVHAPRTTFLESPTSDH	300		
DB	241	NETSHOTSRLRTINSSDDSGKQISCVAMENVGEODSNTLVHAPRTTFLESPTSDH	300		
QY	301	WCIPPTVAGNPKPALQWFGNGLINESKICYIKIHYTHTEYHGCLODNPYHANNQDYT	360		
DB	301	WCIPPTVAGNPKPALQWFGNGLINESKICYIKIHYTHTEYHGCLODNPYHANNQDYT	360		
QY	361	LIAKNEYKDEKQOISAHFMGWPBGIDGANPNYPDYIYBDYGTANDIGDTNRSNEIPST	420		
DB	361	IMAKNEYKDEKQOISAHFMGWPBGVYENPNYPDYIYEDWM-TTPDIDIGDTNKSNEIPST	419		
QY	421	DYDTKGTEHLSVAVVWVYIASVVGCLVYMLFLTLAHSKSGMGSPASVISNDSDSAP	480		
DB	420	DVADQTNREHLSVAVVWVYIASVVGCLVYMLLLTLAHSKSGMGSPASVISNDSDSAP	479		
QY	481	LHHSNGSNTSPSSSEGGPDVAIIGMTKIPVIENTPOYFGITNSQLKPDFTVOHIGKNIVL	540		
DB	480	LHHSNGSNTSPSSSEGGPDVAIIGMTKIPVIENTPOYFGITNSQLKPDFTVOHIGKNIVL	539		
QY	541	KRELGEAGFKGVFLAECYNLCPEODKILVAVTTLXSDASDNARKDFFREAEILLTNLOHEHI	600		
DB	540	KRELGEAGFKGVFLAECYNLCPEODKILVAVTTLXSDASDNARKDFFREAEILLTNLOHEHI	599		
QY	601	VKFYVAVCEGDPILINVFETMKRGDLANKFLRANGPDVAIYAEENPPTELQSQMLHIAQOI	660		
DB	600	VKFYVAVCEGDPILINVFETMKRGDLANKFLRANGPDVAIYAEENPPTELQSQMLHIAQOI	659		
QY	661	AAGWYLLASQHPVHDLATRNCLVGENILLVKIGDGMSSRDVYSTYRYRGHITMLPIRKM	720		
DB	660	AAGWYLLASQHPVHDLATRNCLVGENILLVKIGDGMSSRDVYSTYRYRGHITMLPIRKM	719		
QY	721	PPESIMYRKFTESDVMSLGVYLMEIFTYQKOPWYOLSNNEYIECTQGRVLORPCTQO	780		
DB	720	PPESIMYRKFTESDVMSLGVYLMEIFTYQKOPWYOLSNNEYIECTQGRVLORPCTQO	779		
QY	781	EYELMLGCMQREPRMKIKIIGITLLQNLAAASPYIIDILG 822			
DB	780	EYELMLGCMQREPRMKIKIIGITLLQNLAAASPYIIDILG 821			
RESULT 5					
IRKB_CHICK					
TRKB_CHICK STANDARD; PRT; 818 AA.					

CC 091987; 091010;  
 CC 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB  
 DE tyrosine kinase) (Trk-B).  
 DN Name=TRKB;  
 OS Gallus gallus (Chicken).  
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 10).  
 RC TISSUE=Brain;  
 RX MEDLINE=95047511; PubMed=7959025; DOI=10.1016/0378-1119(94)90184-8;  
 RA Vinh N., Erdmann K., Heumann R.;  
 RT "Cloning and sequence analysis of a cDNA encoding a novel truncated  
 RT form of the chicken TrkB receptor.";  
 RL Gene 149:383-384 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=94116452; PubMed=8287802;  
 RA Dechant G., Biffo S., Okazawa H., Kolbeck R., Potgiesser J.,  
 RA Barde Y.-A.;  
 RT "Expression and binding characteristics of the BDNF receptor chick  
 RT trkB.";  
 RL Development 119:545-558 (1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE FROM N.A.  
 RP (ISOFORM 2; 3; 4; 5; 6; 7; 8; 9; 10; 11 AND 12).  
 RX MEDLINE=963070546; PubMed=8774442;  
 RA Garner A.S., Menegay H.J., Boeshore K.L., Xie X.Y., Voci J.M.,  
 RA Johnson J.E., Large T.H.;  
 RT "Expression of TrkB receptor isoforms in the developing avian visual  
 RT system.";  
 RL J. Neurosci. 16:1740-1752 (1996).  
 CC -1- FUNCTION: Receptor for brain-derived neurotrophic factor (BDNF),  
 CC neurotrophin-3 and neurotrophin-4/5 but not nerve growth factor  
 CC (NGF). Involved in the development and/or maintenance of the  
 CC nervous system. This is a tyrosine-protein kinase receptor. Known  
 CC substrates for the TRK receptors are Shc1, PI-3 kinase, and PLC-  
 CC gamma-1 (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low  
 CC affinity) and dimeric (high affinity) structures (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=12;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1; Synonyms=Alpha-Fl;  
 CC IsoId=Q91987-1; Sequence=Displayed;  
 CC Name=2; Synonyms=beta-Fl;  
 CC IsoId=Q91987-2; Sequence=VSP\_002914;  
 CC Note=It is uncertain whether Leu-144 or Met-188 is the initiator  
 CC of isoform 2;  
 CC Name=3; Synonyms=ED;  
 CC IsoId=Q91987-3; Sequence=VSP\_002915;  
 CC Name=4; Synonyms=UD;  
 CC IsoId=Q91987-4; Sequence=VSP\_002923;  
 CC Name=5; Synonyms=U1;  
 CC IsoId=Q91987-5; Sequence=VSP\_002920;  
 CC Name=6; Synonyms=Alpha-Fl;  
 CC IsoId=Q91987-6; Sequence=VSP\_002918, VSP\_002913;  
 CC Name=7; Synonyms=U1+Fl;  
 CC IsoId=Q91987-7; Sequence=VSP\_002918, VSP\_002919, VSP\_002920;  
 CC Name=8; Synonyms=U2+Fl;  
 CC IsoId=Q91987-8; Sequence=VSP\_002918, VSP\_002919, VSP\_002921;  
 CC Name=9; Synonyms=ED J2+Fl;  
 CC IsoId=Q91987-9; Sequence=VSP\_002915, VSP\_002918, VSP\_002919,  
 CC VSP\_002921;  
 CC Name=10; Synonyms=J1+J2+Fl;

CC	Isoid=Q91987-10; Sequence=VSP_002918, VSP_002919, VSP_002922;
CC	Name=11; Synonyms=T3;
CC	Isoid=Q91987-11; Sequence=VSP_002916, VSP_002917;
CC	Name=12; Synonyms=ED J1+J2+T1;
CC	Isoid=Q91987-12; Sequence=VSP_002915, VSP_002918, VSP_002919,
CC	VSP_002922;
CC	-1- PTM: Ligand-mediated auto-phosphorylation.
CC	-1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin
CC	receptor subfamily.
CC	-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC	-1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC	-----
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CC	entities requires a license agreement (See <a href="http://www.isb-sdb.ch/announce/">http://www.isb-sdb.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sdb.ch">license@isb-sdb.ch</a> ).
CC	-----
DR	EMBL, X77251; CAA54468.1; -
DR	EMBL, X77252; CAA54469.1; -
DR	EMBL, X74109; CAA52210.1; -
DR	PIR, S59939; S44098.
DR	HSP, Q16620; IKB.
DR	InterPro, IPR011061; Antihaemostatic.
DR	InterPro, IPR007110; Ig-like.
DR	InterPro, IPR011009; Kinase_like.
DR	InterPro, IPR001611; LRR.
DR	InterPro, IPR000719; Prot_kinase.
DR	InterPro, IPR002011; RecepttyrkineH1.
DR	InterPro, IPR001245; Tyr_pkinase.
DR	InterPro, IPR008266; Tyr_pkinase_AS.
DR	Pfam, PF00047; Ig_1.
DR	Pfam, PF00560; LRR; 1.
DR	Pfam, PF00069; Pkinase; 1.
DR	PRINTS, PR00109; TYRKINASE.
DR	ProDom, PDD00001; Prot_kinase; 1.
DR	ProDom, PDS00835; IG_LIKE; 1.
DR	PROSITE, PS001107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE, PS50011; PROTEIN_KINASE_ATP; 1.
DR	PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE, PS00239; RECEPTOR_TYR_KIN_1; 1.
KM	Alternative splicing; ATP-binding; Glycoprotein;
KM	Immunoglobulin domain; Leucine-rich repeat; Neurogenesis;
KM	Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;
KM	Tyrosine-protein kinase.
FT	SIGNAL 1 31
FT	CHAIN 32 818
FT	DOMAIN 32 426
FT	TRANSMEM 427 450
FT	DOMAIN 451 818
FT	REPEAT 71 92
FT	REPEAT 95 116
FT	DOMAIN 126 281
FT	DOMAIN 295 364
FT	DOMAIN 344 803
FT	NP_BIND 540 548
FT	BINDING 548 568
FT	ACT_SITE 672 672
FT	DISULFID 32 38
FT	DISULFID 36 45
FT	DISULFID 151 175
FT	DISULFID 153 193
FT	DISULFID 217 265
FT	DISULFID 301 344
FT	MOD_RES 512 512
FT	MOD_RES 698 698
FT	MOD_RES 702 702
FT	MOD_RES 703 703
FT	MOD_RES 703 703

FT	MOD_RES	813	813	similarity).
FT				Phosphotyrosine (by autocatalysis) (By
FT	SITE	512	512	similarity).
FT	SITE	813	813	Interaction with SHC1 (By similarity).
FT				Interaction with PLC-gamma-1 (By
FT				similarity).
FT	CARBOHYD	66	66	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	94	94	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	120	120	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	199	199	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	204	204	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	226	226	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	253	253	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	287	287	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	324	324	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	337	337	N-linked (GlcNAc . . .) (potential).
FT	CARBOHYD	408	408	N-linked (GlcNAc . . .) (potential).
FT	VARSPLIC	1	187	Missing (in isoform 2).
FT				/FTId=VSP_002914.
FT	VARSPLIC	384	394	Missing (in isoform 3, isoform 9 and
FT				isoform 12).
FT				/FTId=VSP_002915.
FT	VARSPLIC	462	467	GPSY1 -> ERGRK (in isoform 11).
FT				/FTId=VSP_002916.
FT	VARSPLIC	468	818	Missing (in isoform 11).
FT				/FTId=VSP_002917.
FT	VARSPLIC	463	473	PSSVSNDDDS -> FVLEFKIPLDG (in isoform 6,
FT				isoform 7, isoform 8, isoform 9, isoform
FT				10 and isoform 12).
FT				/FTId=VSP_002918.
FT	VARSPLIC	474	818	Missing (in isoform 6, isoform 7, isoform
FT				8, isoform 9, isoform 10 and isoform 12).
FT				/FTId=VSP_002919.
FT	VARSPLIC	462	462	G -> VHGSEVKGVLVDQIWLISLQDCNDEBG (in
FT				isoform 5 and isoform 7).
FT				/FTId=VSP_002920.
FT	VARSPLIC	462	462	G -> EQVMATVNSDVHNNSTASDNNRLG (in isoform
FT				8 and isoform 9).
FT				/FTId=VSP_002921.
FT	VARSPLIC	462	462	G -> VHGSEVKGVLVDQIWLISLQDCNDEBGVTVNSDVH
FT				NNSTASDNNRLG (in isoform 10 and isoform
FT				12).
FT				/FTId=VSP_002922.
FT	VARSPLIC	462	465	Missing (in isoform 4).
FT				/FTId=VSP_002923.
FT	SEQUENCE	818 AA;	91736 MW;	D1BA39E2092B2152 CRC64;
Query Match		77.5%;	Score 3426;	DB 1;
Beet Local Similarity		77.6%;	Pred. No. 8.7e-193;	Length 818;
Matches 638;	Conservative	73;	Mismatches 107;	Indels 4;
				Gaps 3
QY				1 MSWIRMGPAWAKRMGFCMLVGFMRRAAFAPPTSCSKSASRISCSDPSPGIVAFRLRP 60
DB				1 MYSWRRRRPGGLARLMGLCCVLGCKRQALGCPACRCRSGSKWIKCSRPFGITSPF-VQ 59
QY				61 NSVDENITTEIFIANQKLEIINEDVEAYVGLRNLTVIVDSGLKPYAHKAFKNSNLQHI 120
DB				60 RSTEDDVTETIYIANQRKLESINDNBVGYPVGLKULTVVDSGLRFVSRQAFYKINLYXI 119
QY				121 NFRTRKLTSLSRKHRRHLDSELLIVGNPFTSCDIMTKTIOEAKSSPDYDLYLANS 180
DB				120 NLSRKLKLSLKKPRHGLSLDILVNDPFKSCBETMLKKQOETFYFEADIDYCVDN 179
QY				181 SKNIPPLANQINCGLPSSANLAPLVLYBGRKISITLSCVADPVDNMVMDVGNVSKM 240
DB				180 NKRIAMDKAKPNCPLPSANLSTNNVITVVGISITLYCDTGGPRPNVSMVLNLVSNHE 239
QY				241 NETSHQSLRTINISDSDGKQISCVANLVGEDODSVNLTVHFAPTITFLESPTSDH 3000
DB				240 SOTSNGRPSLTIKYNVSSMDSGIMISCVANLVGEVQTSALTVFAFNITTFIESPTPDH 299
QY				301 WCIPFTVGNPKPALQWFLYNGAILNBSKYITCKIHVYTNHTEVHGCLQDNDPTNNNGDYT 360



Db 300 WCIFPTKGNKPKPLQWFBGAIINBSRYICTKHVINOSEHYGCLQDNPHTLANKAVT 359  
 Qy 361 LIANREYGEDEKQISAFHEWMPGIDDGANPNYPVIEYEDYGTANDIGDTNRSENEIPST 420  
 Db 360 LIANREYGEDEKRDADAHMSVPG--DSSGPIVDDPYVE-YETTTNDIGDTNNNSQITSP 416  
 Qy 421 DVTDKTGREHLISYAVAVVIASVVGFCILVMLFLKLARHSFKMGKSPASVISNDDASAP 480  
 Db 417 DVSNKREHDSITVYVWVVGIALVCTGLVIMLIILKFGHRSFKGMKGFSSVISNDDASAP 476  
 Qy 481 LHHISNSNTPSSSEGGPDVAITGMTKIPVLEENPOYRITTSOLKPDFFVGHIRHNIVL 540  
 Db 477 LHHISNSNTPSSSEGGPDVAITGMTKIPVLEENPOYRITTSOLKPDFFVGHIRHNIVL 536  
 Qy 541 KRELGEAGFGKVFALAEACYNLCPEODKILVAVKTLKQASDNARKDFHRAELITNLQHEHI 600  
 Db 537 KRELGEAGFGKVFALAEACYNLCPEODKILVAVKTLKQASDNARKDFHRAELITNLQHEHI 596  
 Qy 601 VKFYGVCEGDDPLIMVEFYMKHGDNLKFLRAHGPDAVLAEGNPTELITQSOMLHIAQOI 660  
 Db 597 VKFYGVCEGDDPLIMVEFYMKHGDNLKFLRAHGPDAVLAEGNPTELITQSOMLHIAQOI 656  
 Qy 661 AAGNVIYLAHQFVHRDLATRNCLVGENILVKIGDPMGRSDYSTDYRVGHTMLPIRM 720  
 Db 657 AAGNVIYLAHQFVHRDLATRNCLVGENILVKIGDPMGRSDYSTDYRVGHTMLPIRM 716  
 Qy 721 PPSIMTRKFTTESDVSIGVVLWEIFTYKGQPMYQLSNNEVEICTTGQVLOPRTPQ 780  
 Db 717 PPSIMTRKFTTESDVSIGVVLWEIFTYKGQPMYQLSNNEVEICTTGQVLOPRTPQ 776  
 Qy 781 EVELMLGCWQREBPMRNKINGIHTLLQNLAKASPVYLDILG 822  
 Db 777 EYVDLMGCWQREBPMRNKINGIHTLLQNLAKASPVYLDILG 818

RESULT 6  
 QYTH44 PRELIMINARY, PRT, 821 AA.  
 AC QYTH44  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)  
 DE Neurotrophin receptor B xtrkb-alpha.  
 GN Name=xtrkb;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NC NCB1\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97101727; PubMed=8946245;  
 RA Islam N., Gagnon F., Moss T.;  
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
 mRNA are expressed in a pseudo-segmental manner within the early  
 RT Xenopus central nervous system.";  
 RL Int. J. Dev. Biol. 40:973-983(1996).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin  
 CC receptor subfamily.  
 DR EMBL: U39670; AAD00001.1; -;  
 DR HSBP; O16620; IWB  
 DR GO: GO:00016021; C: integral to membrane; IEA.  
 DR GO: GO:0005524; F: ATP binding; IEA.  
 DR GO: GO:0004872; F: receptor activity; IEA.  
 DR GO: GO:0016740; F: transferase activity; IEA.  
 DR GO: GO:0004714; F: transmembrane receptor tyrosine kin. . .; IEA.  
 DR GO: GO:0006468; P: protein amino acid phosphorylation; IEA.  
 DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR011009; Kinase\_like.

DR InterPro; IPR000483; IAR\_Cterm.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002011; ReceptctykinasII.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008265; Tyr\_kinase\_AS.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00082; LRCT; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 KW ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;  
 KW Transmembrane; Tyrosine-protein kinase.  
 SQ SEQUENCE 821 AA; 92311 MW; 0AF81BE74FDBFED3 CRC64;

Query Match 70.0%; Score 3091.5; DB 2; Length 821;  
 Best Local Similarity 71.5%; Pred. No. 3.8e-173;  
 Matches 591; Conservative 88; Mismatches 137; Indels 11; Gaps 9;

Qy 1 MSSWIRHGGPAMARLMGFCWLVG-FWRAPACPTCKCSASRIWCSDPSCGIVAPRLB 59  
 Db 1 MRLMKSGHGPDLVEVYGALWILALFWR-GLACPQYCSNSTRITWCTLMDKGIAPVLB 59  
 Qy 60 PNVSDPENITIEIFRANQKRLIINEDDEAVVGIKILTIYDSGLKFAVAKAFKRSNQH 119  
 Db 60 DSSL-AENITIDIVIANORSLASINDDVKIYTGRLNLTVDSGIATVSRQAFRNKLKLT 118  
 Qy 120 INFRNKLTSLSRGFPHLDSEILVGNPPTSCSDIMWIKTLQBAKS-SPDTQDLYCLN 178  
 Db 119 INFSRNLTSLSITKIFPHLTLSQLLGPNPQSCDLMMVAVVLETSSINENONHFN 178  
 Qy 179 ESSKNIPLANLIQIPNCGIPSNALAPNLVYBEGSITLSCSVAGDPVPMYVGNLVSK 238  
 Db 179 DNKKKIPLENMHIPOGPIANVSTVNIYVLEGNETTLYCDANGLPDPMWMDISQITSK 238  
 Qy 239 HMMTSHTQSLRTTNISSSDSGKOISCVANLVGEODSVNLVHPAPTTPLESPTSD 298  
 Db 239 KRMMAKRPVLLTLKNVTSLDNKKRIIVCANVNSGEBHISVELNVHPVPTTFIDLPID 298  
 Qy 299 HMMCIPTVGNPNPVALOMFPNGAILNESKVICIKIYVTHN--TEYGCQLDNPTRHNN 356  
 Db 299 HMMCIPTSVKGNPFTLOMFHEGILSTIDPFWSKIHETSYTSEHGCLOLDSPTLNN 358  
 Qy 357 GDVTLAKNEYGEDEKQISAFHEWMPGIDDGANPNYPVIEYEDYGTANDIGDT-TNRSN 415  
 Db 359 GFYTLRAENIYGRBERSIALFMKGP--DGS-NP-ITDPGYVDYETTSNDIGSTDTIGT 414  
 Qy 416 EIPSTDVDTKGRHLSYAVAVVIASVVGFCILVMLFLKLARHSFKMGKSPASVISND 475  
 Db 415 GVTSTDVNSNGENBSITVYVWVVGIALVCTGLVIMLIILKFGHRSFKGLKPPSSVISND 474  
 Qy 476 DSAELHHSNGSTPSSSEGGPDVAITGMTKIPVLEENPOYRITTSOLKPDFFVGHIR 535  
 Db 475 DSAELHHSNGSTPSSSEGGPDVAITGMTKIPVLEENPOYRITTSOLKPDFFVGHIR 534  
 Qy 536 HNIYLAKELEGAGKVFALAEACYNLCPEODKILVAVKTLKQASDNARKDFHRAELITNL 595  
 Db 535 HNIYLAKELEGAGKVFALAEACYNLCPEODKILVAVKTLKQASDNARKDFHRAELITNL 594  
 Qy 596 QHEHIVFYGVCEGDDPLIMVEFYMKHGDNLKFLRAHGPDAVLAEGNPTELITQSOMLH 655  
 Db 595 QHEHIVFYGVCEGDDPLIMVEFYMKHGDNLKFLRAHGPDAVLAEGNPTELITQSOMLH 654  
 Qy 656 IAAQIIAAGMYTIAHQFVHRDLATRNCLVGENILVKIGDPMGRSDYSTDYRVGHTML 715  
 Db 655 IAAQIIAAGMYTIAHQFVHRDLATRNCLVGENILVKIGDPMGRSDYSTDYRVGHTML 714  
 Qy 716 PIRMPPEISIMYRKFTTESDVSIGVVLWEIFTYKGQPMYQLSNNEVEICTTGQVLOPR 775



Db 715 PIRMPPEESIMYKRTTESDVMSLGVLMELFTYGKOPWYQLSNNEVIECTGQVLRP 774  
 QY 776 RTCPQVEYELMLGCMQREPHMRKNIKGIHTLLQNLAAASPVYLDIIG 822  
 Db 775 RTCPKEVYDMLGCMQREPHMRKNIKGIHTLLQNLAAASPVYLDIIG 821

RESULT 7  
 QYH43 PRELIMINARY; PRT; 811 AA.  
 ID QYH43  
 AC QYH43;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Neurotrophin receptor B xtrkb-alpha.  
 GN Name=xtrkb;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae, Pipridae;  
 OC Xenopodidae; Xenopus.  
 ON NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97101727; PubMed=8946245;  
 RA Islam N., Gagnon F., Moss T.;  
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
 mRNA are expressed in a pseudo-segmental manner within the early  
 RT Xenopus central nervous system.";  
 RL Int. J. Dev. Biol. 40:973-983(1996).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin  
 CC receptor subfamily.  
 CC EMBL; U39671; AAD00002.1; -.  
 DR HSSP; Q16620; 1MB.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.  
 DR Interpro; IPR003599; IG.  
 DR Interpro; IPR007110; IG-like.  
 DR Interpro; IPR011009; Kinase\_1like.  
 DR Interpro; IPR000483; LRR\_Cterm.  
 DR Interpro; IPR000719; Prot\_kinase.  
 DR Interpro; IPR002011; Recepttyrkinasit.  
 DR Interpro; IPR001245; Tyr\_kinase.  
 DR Interpro; IPR008266; Tyr\_kinase\_AS.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00409; IG\_1\_kinase; 1.  
 DR SMART; SM00082; LRCT; 1.  
 DR SMART; SM00219; TYK; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR TYR\_KIN\_1; 1.  
 KW ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;  
 KW Transmembrane; Tyrosine-protein kinase.  
 SQ SQUENCE 811 AA; 91249 MW; CE7CDICF132C1CFS CRC64;

Query Match 69.7%; Score 3078.5; DB 2; Length 811;  
 Best Local Similarity 71.0%; Pred. No. 2.2e-172;  
 Matches 587; Conservative 87; Mismatches 132; Indels 21; Gaps 8;

QY 1 MSSVIRHMGAMARLWGFCLVVG-FVRAAFACPTSCGASRSRISDPSFGVAFPRLE 59  
 Db 1 MRLMKSGHGDVLEVYGAATLILAFWR-GLACQYSCSCTRIMCTLMKXGIAAFVLE 59  
 QY 60 PMSVDPENITEIFIANOKRLIINEDVEAYVGLRLITVDSGLKFAVAKFLKNSLQH 119

Db 60 DSSL-ABENTIDITYANORSLASINDDVKTITGRLITVDSGLQVSRAPFRKNTLTY 118  
 QY 120 INFRNKLTSLSRKFRHLDLSELIVGNPFTSCDIMIKTLQOKAS-SPTDPLYCLN 178  
 Db 119 INFSRNKLTSLTKIFRHLTSLQLLGQNFQSCDLMVKVLEJTNLSLMENONHICFN 178  
 QY 179 ESSKNTPLANLQIPNGCLPBANLAPRLTYEKGSLTSGSVAGDPVNNMYDGNLVS 238  
 Db 179 DNKKIPLFNMHLPNGCLPTANVSTVITLBNETTLVCDANGLPDPNWSMDI8Q119K 238  
 QY 239 HNMETSHQSLRTITVSSPDGKOISCVANLVGSDSVNLTVPAPITFLSPSTP 298  
 Db 239 KRMEMAKRPVLLTKVNTSLDNKRITVCANESVGDHISVELANVFPPIITLIDPLTD 298  
 QY 299 HNMCIPTVGNKPKPALOMFYNGAIIINESKYICTKIHTNH--TEYHGLQDNPPTMMN 356  
 Db 299 HNMCIPTVGNKPKPALOMFYNGAIIINESKYICTKIHTNH--TEYHGLQDNPPTMMN 356  
 QY 357 GDTTLAKNEYGKDEKQISAHFNGWPEIDGAPNPTPDVYEDYGRANDIGDT-TKSN 415  
 Db 359 GFTYLAENITVGRDEKISALFMKGP--DD-----DYETTSNDIGGSTDICT 404  
 QY 416 EIPSTDTDKTGRHEHLSVAVVVIASVYGRCLVWLFLKLARHSKGMKGPASVIND 475  
 Db 405 GVTSTVDSNGNEDSITVYVVGIALVCTGLVIMLILFGHSHKFGKLGSPSVSND 464  
 QY 476 DSASPLHISNGSNTSSSEGGPDVAIVGTIKTPIVLENPQYFGITNSQLPDPFVQHKR 535  
 Db 465 DSASPLHISNGSNTSSSEGGPDVYIGTKPIVLENPQYFGITNSQLPDPFVQHKR 524  
 QY 536 HNIYLRKELEGAPFGVFLAECYNLCPEODKILVAVKTLKQASDNARKDPRERAEILTNL 595  
 Db 525 HNIYLRKELEGAPFGVFLAECYNLCPEODKILVAVKTLKQASDNARKDPRERAEILTNL 584  
 QY 596 QHEHIVKFGVCEGDPILVVFYMKRGDKNFKLRAHGPVAVMARGNPTELTOGOMLH 655  
 Db 585 QHEHIVKFGVCEGDPILVVFYMKRGDKNFKLRAHGPVAVMARGNPTELTOGOMLH 644  
 QY 656 IAQIAGWVYLLASQHFVHDLATRNCLVGENLVKIGDFGMSRDVYSTDYRGHHTML 715  
 Db 645 IAQIAGWVYLLASQHFVHDLATRNCLVGENLVKIGDFGMSRDVYSTDYRGHHTML 704  
 QY 716 PIRMPPEESIMYKRTTESDVMSLGVLMELFTYGKOPWYQLSNNEVIECTGQVLRP 775  
 Db 705 PIRMPPEESIMYKRTTESDVMSLGVLMELFTYGKOPWYQLSNNEVIECTGQVLRP 764  
 QY 776 RTCPQVEYELMLGCMQREPHMRKNIKGIHTLLQNLAAASPVYLDIIG 822  
 Db 765 RTCPKEVYDMLGCMQREPHMRKNIKGIHTLLQNLAAASPVYLDIIG 811

RESULT 8  
 QYH43 PRELIMINARY; PRT; 669 AA.  
 ID QYH43  
 AC QYH43;  
 DT 25-OCT-2004 (TREMblrel. 28, Created)  
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)  
 DE Tyrosine kinase receptor (Fragment).  
 OS Peophila guttata (Zebra finch) (Taeniopygia guttata).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;  
 OC Estrildinae; Taeniopygia.  
 ON NCBI\_TaxID=59729;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Agate R.J., Chen X., Itch Y., Arnold A.P.;  
 RT "Cloning and expression of trkb in zebra finch brain.";  
 RN Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RA Thompson J.F.;

RL Submitted (UTL-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin  
CC receptor subfamily.  
DR EMBL: AF69520; AAT8083.1; -  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR003599; IG-like.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_c2.  
DR InterPro: IPR011009; Kinase like.  
DR InterPro: IPR000719; Prot\_kinase.  
DR InterPro: IPR002011; ReceptLtyrkinasII.  
DR InterPro: IPR002290; Ser\_chr\_kinase.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR InterPro: IPR008266; Tyr\_kinase\_AS.  
DR Pfam: PF00047; Ig; 1.  
DR Pfam: PF00069; Kinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00409; IG; 1.  
DR SMART: SM00408; IGc2; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR SMART: SM00219; TYKC; 1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00109; PROTEIN KINASE\_TYR; 1.  
DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
DR ATP-binding; Kinase; Phosphorylation; Receptor; Transferase;  
KW Transmembrane.  
FT NON TER 1 1  
SQ SEQUENCE 669 AA; 74749 MW; 8CA583205F76E269 CRC64;  
  
Query Match 65.5%; Score 2896.5; DB 2; Length 669;  
Best Local Similarity 80.5%; Pred. No. 8.3e-162;  
Matches 540; Conservative 48; Mismatches 80; Indels 3; Gaps 2;  
  
QY 152 CSDIMIMIKTLOEAKSSPDGDLCLINSSKNIPLANQIPNCGLPANLAAPIUTYEEG 211  
DB 2 CSCIMIMIKRQETKFTYETDLYCVDNNKKTALLDMKVPNCPLPSANLNYITVEG 61  
QY 212 KSITLSCSVAGDPVPMYWDVGNLVSXKIMETSHTOGSLRTINISDSGKQISCVENL 271  
DB 62 KSITLYCDTGGPPPNVSWVTNLVSNHESDTNKNPASTLTKVNSMDSGLISCVENI 121  
QY 272 VGEQDSVNLTVHAPRTTPELESPTSDDHWCIPPTVKGNPKPALQWFTYNGAILNESKYIC 331  
DB 122 VGEQDASAEALVFPAPNITFTIESPTPDHWCIPFTVKGNPKPTLQWFEAGVAINESBYIC 181  
QY 332 TKIHVHTTEYHGLQIDNPFTMNGDVTLLAKNEYGDEKQISAHFMGWDGIDGANPN 391  
DB 182 TKIHVHIOSEYHGLQIDNPFTLNNGATLLAKNDYGEDKRVDFHFSVGG--DGNQPI 239  
QY 392 YPDVIEDYGTAAIDGDTTNRSEIPESTDVDTKGTREHLSVYAVVAVLASVGFCLVWL 451  
DB 240 LDPDYVE-YETTPDLDGATNNSNOISTDVSNKENESITVYVVVGIALVCGIIVTL 298  
QY 452 FLTLAHSKFGKMGKPAVISNDDSDASPLHISNGSTPSSSGGPDVAIIIGWTKIPVI 511  
DB 299 IILFGHSHSKFGKMGKPAVISNDDSDASPLHISNGSTPSSSGGPDVAIIIGWTKIPVI 358  
QY 512 ENPQYFGTNSQLKPDFTVQHIKRNHNYLXRELSEGAAGKVFALAEVNLCEQDOKIIVAV 571  
DB 359 ENPQYFGTNSQLKPDFTVHIIKRNHNYLXRELSEGAAGKVFALAEVNLCEQDOKIIVAV 418  
QY 572 KTLKADSDNAKDKPHREAEALLTNLQHEHIVFYGVCVEGDPDLMVFETMKHGDLNKFURA 631

DB 419 KTLKADSDNAKDKPHREAEALLTNLQHEHIVFYGVCVEGDPDLMVFETMKHGDLNKFURA 478  
QY 632 HGPDAVMAEGNPTEITLOSOMLHIAQOIAAGWYILASQHVHDLATRNCLVGENILYK 691  
DB 479 HGPDAVMAEGNPTEITLOSOMLHIAQOIAAGWYILASQHVHDLATRNCLVGENILYK 538  
QY 692 IGDGMSRDVYSTDYVEVGHITMLPIRMMPESIMYRKFTTESDVSLSGVLMELFTYK 751  
DB 539 IGDGMSRDVYSTDYVEVGHITMLPIRMMPESIMYRKFTTESDVSLSGVLMELFTYK 598  
QY 752 QPWYLSNNEVEICTIGRVLQRPRTCPQEVYELMLGCMQREPHRNKXIKIHTLLQVLA 811  
DB 599 QPWYLSNNEVEICTIGRVLQRPRTCPKEVYDMLGCMQREPHRNKXIKIHTLLQVLA 658  
QY 812 KASPVYDILG 822  
DB 659 KASPVYDILG 669  
  
RESULT 9  
Q8WKJ5 PRELIMINARY; PRT; 553 AA.  
ID Q8WKJ5  
AC Q8WKJ5;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
GN Neurotrophin receptor tyrosine kinase type 2 truncated isoform.  
GN Name=NTKR2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINB=21656983; PubMed=11798182;  
RA Stoilov P., Castren E., Stamm S.;  
RT "Analysis of the human TrkB gene genomic organization reveals novel  
RT TrkB isoforms, unusual gene length, and splicing mechanism.";  
RL Biochem. Biophys. Res. Commun. 290:1054-1065(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Stoilov P.G., Castren E., Stamm S.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF410901; AAL67967.1; -  
DR HSP; Q16620; IAMB.  
DR GO: GO:0016301; F:kinase activity; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR Pfam: PF01462; LRRTY; 1.  
DR SMART: SM00408; IGc2; 1.  
DR SMART: SM00082; LRRTY; 1.  
DR SMART: SM00013; LRRTY; 1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
KW Kinase; Receptor.  
SQ SEQUENCE 553 AA; 60993 MW; BD98221B9EB1A6C1 CRC64;  
  
Query Match 64.0%; Score 2826; DB 2; Length 553;  
Best Local Similarity 96.9%; Pred. No. 9e-158;  
Matches 528; Conservative 1; Mismatches 0; Indels 16; Gaps 1;  
  
QY 1 MSSWIRHNGPAMARLWGFCLVGFMAFAFCPTSCSKASRIWCSPPGIVAFPRLEP 60  
DB 1 MSSWIRHNGPAMARLWGFCLVGFMAFAFCPTSCSKASRIWCSPPGIVAFPRLEP 60  
QY 61 NSVDPENITETPIANQRLBITNEDVYAYVGLNLTIVDSGLKFAVHAKAFLKSNLQHI 120  
DB 61 NSVDPENITETPIANQRLBITNEDVYAYVGLNLTIVDSGLKFAVHAKAFLKSNLQHI 120  
QY 121 NFRNKTLSLSRGRFRLLDSELILVNGNPTSCSDIMWIKTLOAKSSPDQDLYCLNES 180  
DB 121 NFRNKTLSLSRGRFRRLDSELILVNGNPTSCSDIMWIKTLOAKSSPDQDLYCLNES 180  
QY 181 SKNIPLANQIPNCGLPANLAAPIUTYEEG 211

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DB 181 SKIPLPLANLIPNCGLPSPALMAAPNLVEBGSKITLSSCSVAAGDPVPMYMDVGNLSKAM 240
QY 241 NETSHTGSLRITNISSDSGKOISCAVAENLVEGDODSVNLTVFAFTITFLESPTSDH 300
DB 241 NETSHTGSLRITNISSDSGKOISCAVAENLVEGDODSVNLTVFAFTITFLESPTSDH 300
QY 301 WCIPFYKGNPKPALQWFFNGALINEBKYCTKHVNTNHEHYGCLQDNPMTMANGDYT 360
DB 301 WCIPFYKGNPKPALQWFFNGALINEBKYCTKHVNTNHEHYGCLQDNPMTMANGDYT 360
QY 361 LIANKEXGDEKOKSAHFMCMPGIDGDPANPNYPVYEDYGTANDIGDTTNSNEIPST 420
DB 361 LIANKEXGDEKOKSAHFMCMPGIDGDPANPNYPVYEDYGTANDIGDTTNSNEIPST 420
QY 421 DVTDKTGREHLISVYAVVVIASVVGFCLLVNLFLKLARHSKFGMK----- 465
DB 421 DVTDKTGREHLISVYAVVVIASVVGFCLLVNLFLKLARHSKFGMKDPWFPGKVSROG 480
QY 466 -GPASVSNDDDSAPLHHSNCSNTSSSGGPDVITGMTKIPIVENPOYFGITNSOL 524
DB 466 -GPASVSNDDDSAPLHHSNCSNTSSSGGPDVITGMTKIPIVENPOYFGITNSOL 540
QY 525 KPPTF 529
DB 541 KPDTW 545

RESULT 10
06VNS1 PRELIMINARY; PRT; 825 AA.
AC QCVNS1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Neurotrophic tyrosine kinase receptor.
GN Name-trkC;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=14614136; DOI=10.1073/pnas.2336152100;
RA Yamauchi J., Chan J.R., Shooter E.M.;
RT "Neurotrophin 3 activation of TrkC induces Schwann cell migration
RT through the c-Jun N-terminal kinase pathway."
RL Proc Natl. Acad. Sci. U.S.A. 100:14421-14426(2003).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
DR EMBL; AY336094; AAP94280.1; -.
DR HSSP; P08069; IKA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR011009; kinase_like.
DR InterPro; IPR016111; LRR.
DR InterPro; IPR00483; LRR_Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; ReceptTykKinse.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; 1g; 1.
DR Pfam; PF00462; LRRNT; 1.
DR Pfam; PF00560; LRR_1; 2.
DR PRINTS; PR00019; LEURICHRPT.
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DR PRINTS; PR00019; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TykC; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_1; 1.
DR APP-binding; Kinase; Phosphorylation; Receptor; Transferase;
KW Transmembrane.
SQ SEQUENCE 825 AA; 92760 MW; 4DE08AB546CC5BD6 CRC64;

Query Match 52.0%; Score 2296; DB 2; Length 825;
Best local similarity 55.0%; Pred. No. 2e-126;
Matches 468; Conservative 107; Mismatches 206; Indels 70; Gaps 16;

QY 10 PAMARL-----GFCWL-VVGFRAAFACPTSCKSASRIWCSDPSPGIVAFRLP--- 60
DB 7 PAKCFMRIFILGSVMDYVG---SVLACPANCVCSTKTEINCRPPDGNL-FLLBQDS 62
QY 61 -----NSVD-PENITEIFIANOKLEIINEDDVEAVVGRNLTIVDSGLKFAHKA 110
DB 63 GNSGNASINITIDISRNITSIHENRGLHTLAIVMEIYGLQKLTNNSGLRNIOGRA 122
QY 111 FLKNSNLQHNIFRNKLTLSRRKPHRLDSEILVGNPFTCSQDIMIKITLQE-AKSP 169
DB 123 FALNPHLRYNLSNNLTLSMQLPOTLSRELRLEQNFNGSCDILRMQWLMQEQEARL 182
QY 170 DTQDLYCLNESSKNIPLANLIQPNCGLPANLAPNLVEBGSKITLSSVAGDPVPMY 229
DB 183 DSQSLVCSHDSQQLPLFRNRIQCDLPBISVSHVNLTVBGNNAVITCNGSGSPDPVD 242
QY 230 WDVGNLVS-----KHNERSHTGSLRITNISSDSGKOISCAVAENLVEGDODSVNLTV 284
DB 243 WITYGQISNTQNTNMTNVAHINTLVNVTSEDDGFTLTCAENNVGNSNVALTVY 302
QY 285 FAPTITFLESPTSDHMCIPFTVGNPKPALQWFFNGALINEBKYCTKHVNTNHEHYH- 343
DB 303 YPRVIVSLVEPRVRLHCHIEFVVRGNPPTLTALHLYNGQPLREBKII-----HNDYQ 354
QY 344 -----GCLQDNPMTMANGDYTLIAKXEGDEKOKISAHFMCGPIDGDPANPNYPDVIY 397
DB 355 EGEVSEGLLFNKPFTYNNNGNYTLIAKNALGTANQTINGHFLKEP-----FPE--- 402
QY 398 EDVGTANDIGDTTNSNEIPSTDYDVKGRHELSYAVVVIASVVGFC-LVNLFL-- 454
DB 403 -----STPFDSESDASPTPTVTTHKPBBDTFGVSIAGLAFA--CVLLVLFPTMIN 454
QY 455 KLARHSKFGMKGPASVSNDDDSAPLHHSNCSNTSSSGGPDVITGMTKIPIVENP 514
DB 455 KYGRSKFKGKGVVAISGEEDSAPLHHSNHTTPSSLDADPDVITGMTKIPIVENP 514
QY 515 QYFGITNSQKPDPTVOHIKRHNIIVLKRELSGAFGKVFILASCYNLCPEDOKILVAVKTL 574
DB 515 QYFRQGNCHKPDPTVOHIKRDIIVLKRELSGAFGKVFILASCYNLSPDKMLVAVKAL 574
QY 575 KDSADNARKDFFHBEALITLVQHEHYKPYGCVBEGDPLINVEYMKGDLNFLRAHGP 634
DB 575 KDPTLAARKDFFHBEALITLVQHEHYKPYGCVBEGDPLINVEYMKGDLNFLRAHGP 634
QY 635 DAVLMAAGNP---PTELTOSQMLHIQOIAAGVNYLASQHFVRDLATRCVGENLTVK 691
DB 635 DAVLTVDGQPRQAKGBLGSQMLHISQLSGWNVYLASQHFVRDLATRCVGENLTVK 694
QY 692 IGFPGMSRDVSYDYRVVGHNTMLPIRMPPBSIMYRKFTTESDVSIGAVLWEIFTYGK 751
DB 695 IGFPGMSRDVSYDYRVVGHNTMLPIRMPPBSIMYRKFTTESDVSIGAVLWEIFTYGK 754
QY 752 QPMYQLSNNEVICITQGRVLAQRPRTCQREYELMLGQWQREPMRKNIGIHTLQNL 811
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Db      755 QPWFQLSNTEVTEICTTGSRVLRPRVCKEYVDWLGCMQREPORLNIKEIKYLHMLG 814
Qy      812 KASPVYDLILG 822
Db      815 KATPIYDILG 825

RESULT 11
Q080WU0 PRELIMINARY; PRT; 476 AA.
ID Q080WU0
AC Q080WU0
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Neurotrophic tyrosine kinase, receptor, type 2.
GN Name=Ntrk2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R., Collins F.S., Wagner L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatcenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Ueda T.B., Toshitsugu S., Carrinci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smallus D.E., Schermer A., Schein J.E.,
RA Jones S.U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052014; AAH52014.2;
DR HSSP; Q16620; IMWB.
DR MGD; MGI:97384; Ntrk2.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007631; P:feeding behavior; IMP.
DR GO; GO:0019222; P:regulation of metabolism; IMP.
DR GO; GO:004548; P:retinal rod cell development; IMP.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000483; IRR_Cterm.
DR InterPro; IPR000372; IRR_Nterm.
DR Pfam; PF01462; LRRT; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00082; LRRT; 1.
DR SMART; SM00013; LRRT; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Kinase; Receptor.
SQ SEQUENCE 476 AA; 53185 MW; 20A8B375BD397ACE CRC64;

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Query Match 51.9%; Score 2292.5; DB 2; Length 476;
Best Local Similarity 89.7%; Pred. No. 1.6e-126;
Matches 418; Conservative 27; Mismatches 20; Indels 1; Gaps 1;

Qy      1 MSSWIRHGPAMARLWGCWLVVGFMAFAFCPTSCCKSARICSPDPSPIVAFPRREP 60
Db      1 MSPWLRHGPAMARLWGCWLVVGFMAFAFCPTSCCKSARICSPDPSPIVAFPRREP 60
Qy      61 NSVDPENITTEIFIANQRLIINEDVEAYVGLNLTIVDSGLKFAVKAFLKSNLQHI 120
Db      61 NSVDPENITTEIFIANQRLIINEDVEAYVGLNLTIVDSGLKFAVKAFLKSNLQHI 120
Qy      121 NFRNKLITSRKRRFLDLSEILVGNPPTSCDIDIMIKTLQAKASPTQDIYCLNES 180
Db      121 NFRNKLITSRKRRFLDLSEILVGNPPTSCDIDIMIKTLQAKASPTQDIYCLNES 180
Qy      181 SKNPLANLQIPNCGLSANLAAPNLVESGKSTLTSCVAGDPVPMVMVGNLVSKM 240
Db      181 SKNPLANLQIPNCGLSANLAAPNLVESGKSTLTSCVAGDPVPMVMVGNLVSKM 240
Qy      241 NETSHTOGSLRTITNSSDSDSGKQISVAVENLVGEDQDSVNLTVFAFPTITLESPTS 300
Db      241 NETSHTOGSLRTITNSSDSDSGKQISVAVENLVGEDQDSVNLTVFAFPTITLESPTS 300
Qy      301 WCIPFTVKNPKPALQPFYNGAILNESKYICTKIHTNTHRYGCLQIDNPTNNNGDYT 360
Db      301 WCIPFTVKNPKPALQPFYNGAILNESKYICTKIHTNTHRYGCLQIDNPTNNNGDYT 360
Qy      361 LIANREYKQEKQISAFPMGPGIDGAPRYEDVITYEDTANIDGDTNRNSNEIST 420
Db      361 LIANREYKQEKQISAFPMGPGIDGAPRYEDVITYEDTANIDGDTNRNSNEIST 420
Qy      421 DVTDQREHLSTVAVVAVVAVSVGFCLVLMFLKLRHSKFGKMG 466
Db      421 DVTDQREHLSTVAVVAVVAVSVGFCLVLMFLKLRHSKFGKMG 466
Db      420 DVTDQREHLSTVAVVAVVAVSVGFCLVLMFLKLRHSKFGKMG 465

RESULT 12
TRKC_HUMAN STANDARD; PRT; 839 AA.
ID TRKC_HUMAN
AC Q16288; Q16287; Q16289;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
DE kinase) (GPI45-TrkC) (Trk-C).
GN Name=NTK3; Synonyms=TRK3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=95124473; PubMed=7823156;
RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT "Human trks: molecular cloning, tissue distribution, and expression of
RT extracellular domain immunoadhesins."
RL J. Neurosci. 15:477-491(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND C).
RC TISSUE=Fetal brain;
RX MEDLINE=95104834; PubMed=7806211;
RA McGregor L.M., Baylín S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;
RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal
RT assignment, and evidence for a splice variant."
RL Genomics 22:267-272(1994).
CC -1- FUNCTION: Receptor for neurotrophin-3 (NT-3). This is a tyrosine-
CC protein kinase receptor. Known substrates for the trk receptors
CC are SHC1, PI-3 kinase, and PLCG1. The different isoforms do not
CC have identical signaling properties.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

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CC Tyrosine phosphate.  
 CC -1- SUBUNIT: Exists in a dynamic equilibrium between monomeric (low  
 CC affinity) and dimeric (high affinity) structures (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=4;  
 CC Comment-Additional isoforms seem to exist;  
 CC Name=A;  
 CC IsoId=Q16288-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=Q16288-2; Sequence=VSP\_002925, VSP\_002926;  
 CC Name=C;  
 CC IsoId=Q16288-3; Sequence=VSP\_002927;  
 CC Name=D;  
 CC IsoId=Q16288-4; Sequence=VSP\_002924;  
 CC -1- TISSUE SPECIFICITY: Widely expressed, mainly in the nervous  
 CC tissue. The isoform B is expressed in a relatively large amount in  
 CC the adult brain comparatively to fetal brain.  
 CC -1- PFM: Ligand-mediated auto-phosphorylation.  
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin  
 CC receptor subfamily.  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL: S76475; AAB3311.1; -;  
 CC EMBL: S76476; AAB3312.1; -;  
 CC EMBL: U05012; AAA75374.1; -;  
 CC PIR: I73632; I73632.  
 CC PIR: I73633; I73633.  
 CC PDB: 1WVC; X-ray; A=297-414.  
 CC Genew: HGNC:8033; NTRK3.  
 CC H-InVDB: HIX0012549; -;  
 CC MIM: 191316; -;  
 CC DR GO: GO:0005887; C:intracellular to plasma membrane; TAS.  
 CC DR GO: GO:0005016; P:neurotrophin TRK receptor activity; TAS.  
 CC DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.  
 CC DR InterPro: IPR007110; Ig-like.  
 CC DR InterPro: IPR011009; Kinase\_like.  
 CC DR InterPro: IPR001611; LRR.  
 CC DR InterPro: IPR000483; LRR\_Cterm.  
 CC DR InterPro: IPR000372; LRR\_Nterm.  
 CC DR InterPro: IPR000719; Prot\_Kinase.  
 CC DR InterPro: IPR002011; ReceptTyKinsII.  
 CC DR InterPro: IPR001245; Tyr\_Kinase.  
 CC DR InterPro: IPR008266; Tyr\_Kinase\_AS.  
 CC Pfam: PF00047; Ig\_1.  
 CC Pfam: PF00560; LRR\_2.  
 CC Pfam: PF01462; LRRNT; 1.  
 CC Pfam: PF00069; Kinase; 1.  
 CC PRINTS: PR00019; LEURICHRP.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC PRODOM: PD000001; Prot\_Kinase; 1.  
 CC SMART: SM00409; IG; 1.  
 CC SMART: SM00082; LRRCT; 1.  
 CC SMART: SM00013; LRRNT; 1.  
 CC SMART: SM00219; TyrcK; 1.  
 CC PROSITE: PS50835; IG\_LIKE; 1.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 CC 3D-structure: Alternative splicing; ATP-binding;  
 CC Direct protein sequencing; Glycoprotein; Immunoglobulin domain;  
 CC Leucine-rich repeat; Neurogenesis; Phosphorylation; Receptor; Repeat;

KW Signal; Transferase; Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 31  
 FT CHAIN 32 839  
 FT DOMAIN 32 429  
 FT TRANSMEM 430 453  
 FT DOMAIN 454 839  
 FT REPEAT 102 125  
 FT REPEAT 126 149  
 FT REPEAT 210 300  
 FT DOMAIN 309 382  
 FT DOMAIN 538 839  
 FT NP\_BIND 544 552  
 FT BINDING 572 572  
 FT ACT\_SITE 679 679  
 FT MOD\_RES 516 516  
 FT MOD\_RES 705 705  
 FT MOD\_RES 709 709  
 FT MOD\_RES 710 710  
 FT MOD\_RES 834 834  
 FT SITE 834 834  
 FT CARBOHYD 72 72  
 FT CARBOHYD 79 79  
 FT CARBOHYD 133 133  
 FT CARBOHYD 163 163  
 FT CARBOHYD 203 203  
 FT CARBOHYD 218 218  
 FT CARBOHYD 232 232  
 FT CARBOHYD 259 259  
 FT CARBOHYD 267 267  
 FT CARBOHYD 272 272  
 FT CARBOHYD 294 294  
 FT CARBOHYD 375 375  
 FT CARBOHYD 388 388  
 FT CARBOHYD 402 410  
 FT VARSPLIC 529 612  
 FT VARSPLIC 613 839  
 FT VARSPLIC 712 725  
 FT CONFLICT 70 70  
 FT CONFLICT 635 635  
 FT STRAND 318 326  
 FT STRAND 332 337  
 FT TURN 338 339  
 FT STRAND 340 341  
 FT STRAND 348 354  
 FT STRAND 358 366  
 FT HELIX 370 372  
 FT STRAND 374 382  
 FT TURN 383 384  
 FT STRAND 385 393  
 FT SEQUENCE 839 AA; 94455 MW; 86D965A503B4DDD CRC64;  
 Query Match 51.5%; Score 2277; DB 1; Length 839;  
 Best Local Similarity 53.7%; Pred. No. 2.6e-125;  
 Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;  
 Oy 10 PAMARLW-----GFCWL-VVGFRAAPACPTSCSKSRIYWCSPSPQIVAFPLRP---60  
 Db 7 PAKCSFRIRILGSLVMDYVG---SVLACPRANCVCSTRIINCRRPDDGNL-FPLIBQDS 62

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QY 61 -----NSVD-PENITIFIANQKRLINEDVEAVYGLNLTIVSGLKFVAHKA 110
DB 63 GNSNGNANINITDISRITSIHENMRSIHTLANAVDELYTGLQKTIKNSGLSIOGRA 122
QY 111 FLKSNLQHINFTNKLTSRKHFRLDSELLVGNPFTCSGDIWIKTLQF-AASSP 169
DB 123 FAKSPHRYINLSSNRLTTSWOLFQTLISREQLQLEONFPCSCDIRMOMQOGAKL 182
QY 170 DTODLYCLNENSSKNIPLANLOIPNCGP.SANLAAPNLVEGKSTLSCVAAGPVPNMY 229
DB 183 NSQNLTCYNADGSLPLFRANISQCDLPEISVSHVNLTVRBGNAVITTCNGSSPLPVD 242
QY 230 WDVGNLVS-----KHNETSHQGLRITNISDSQKQISCVANLVGEODSVNLTVH 284
DB 243 WITVGLQSIHTHQNLMTWNVHAINTLVNTVSEDNQFTLTCIAENYVNGSNASVALTVY 302
QY 285 FAPITLESPTSHMHCIPFTYKGNKRALQWYNGALINESKYICUKIHTNHTYH- 343
DB 303 YPPRVVSLSEBELRLERHCEIVVNGNPPPTLHMLHNOPLRESKTI-----HVEYQ 354
QY 344 -----GCLQDNDPTNNGNDYTLIAKREYKDEKOISAHFMWPGIDDGANPVYPD--- 394
DB 355 EGEISEGCLFNKKTHTNNGYTLIAKNPGLSTANQTINGHFLKEP-----FPESST 405
QY 395 --VLYEDYGAANDIGDTYKRSNEIPSTVDTKGRHLSTYAVAVIASVVFCL-LVMT 451
DB 406 NFLIFEDV-----SPTPIYTHKPEEDTFGSIVAGLAFA--CVLVLVL 449
QY 452 FL--KLARSKFGMKGPASYISDDDSAPLHIHSNGSNTSPSSEGGPDVITIGTKIP 509
DB 450 FVMINKYGRSKFKGMPVAVISGEBDSASPLHIHINQITTPSILDAGPDTVVIGMRIP 509
QY 510 VIENPOYFGITNSQKPDTPVOHKKRHIVYKRELGSGAFKGVLAECNYLCEPDOKTIV 569
DB 510 VIENPOYFGROHCHKEPDTVOHKKRDIVKRELGSGAFKGVLAECNYLSPKQXVL 569
QY 570 AVKTLKASDNARKDFREAEELTNLOHEHIVKFGVCEGDPLIMVEYKHSGLNKL 629
DB 570 AVAKLXOPTLARKDFREAEELTNLOHEHIVKFGVCEGDPLIMVEYKHSGLNKL 629
QY 630 RAHGPDVLAEGNP---PTELTSQMLHIAQOIAAGVNYLASGHPYHDIATNCLVGE 686
DB 630 RAHGPDAMIIVDQGPRAKSELGSMHLSQIASGVNYLASGHPYHDIATNCLVGA 689
QY 687 NLVYKIDFGMSRNVSTDYR-----VGGHTMLIRMPPESSIVYRKFTT 732
DB 690 NLVYKIDFGMSRNVSTDYRRLPNPBGNDPCWCEVGHMTLIRMPPESSIVYRKFTT 749
QY 733 ESDVWSLGVVLMELFTYKQOPWYOLSNNEVEICTQGRVLQRPPTCPOEVELMLGCMOR 792
DB 750 ESDVWSRGVILMEIFTYKQOPWYOLSNNEVEICTQGRVLQRPPTCPOEVELMLGCMOR 809
QY 793 EPHMRKNIKGHTLLQNLAKASPYVLDILG 822
DB 810 EPOORLNKEIKYILHAKGATPIYLDILG 839

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RESULT 13

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O75682 PRELIMINARY; PRT; 839 AA.
AC O75682;
DT 01-NOV-1998 (Tremblrel. 08. Created)
DT 01-NOV-1998 (Tremblrel. 08. Last sequence update)
DT 01-NOV-2004 (Tremblrel. 26. Last annotation update)
DE TRKC protein.
GN Name=TRKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=98449483; PubMed=9778053; DOI=10.1038/sj.onc.1202100;

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RA Ichaño N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.;
RT "Genomic characterization of the human trkC gene.";
FL Oncogene 17:1871-1875(1998).
CC -1- CATALYTIC ACTIVITY. ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- Similarity: Belongs to the Tyr family of protein kinases. Insulin
CC receptor subfamily.
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DR EMBL; AJ224
```



```

Db 123 FAKPHRRTYNLSSNRLTTSKQLFQTLRLQLBEQNFNCSDIRMMQJMOEGEAKL 182
Qy 170 DTQDLYCLANESSKIPLANLOIPNCGIPSANLAPNLTVEGKSTLSCVAGDPVPMY 229
Db 183 NSQNLVCYNADGSQLPFRNINISQCDLPEISVSHVNLTVBEGDAVATVCKSGSGPLPDD 242
Qy 230 WQVGNLV-----KHNMTSHQSLATITVSSDPSKQISCVAKNVGSDOSVNLTV 264
Db 243 WITVGLQSIINTHQTNLMTVNHVHALNLTLVNTSDENFLLTCLAEVNGMSNVALTVY 302
Qy 285 FAPTITLESPTSDHMCIPFTVKNKPKPALOMFYNGALINSEKICITKLHTVHTTEYH- 343
Db 303 YPRVNVLEBRLKHEICIEFVRGNRPPLTHMLHNGQPLRESKLT-----HZZYQ 354
Qy 344 -----GCLQDLPFNANNGDYTLIAKXQYKQEKQISAHFMWPGIDGANPNYPD-- 394
Db 355 EGEISEGCLFENKPTHNNNGNYTLIAKQPLGTANQTINGHFLKRP-----FPFESTD 405
Qy 395 --VIEYEGYRANNDIGTTRNSNEIPSTDTDKGRHLSVYAVVAVASVVGFC-LLVNL 451
Db 406 NFLIFDEV-----SPTPTITVTHKPEEDTFGVSIANGLAFA-CVLLVLVL 449
Qy 452 FLU--KLARSKFKMGKPAVVISNDSDASPLHHISNGSNTPSSSEGQPPAVIIGMTKIP 509
Db 450 FVMTNKYGRSKFKMGKPAVVISGEBDSASPLHHINHGITTSSLDAGPDTVVIAMTRIP 509
Qy 510 VIEPNQYFGITNSQLKPDFTVOHAKRNIYVLRKELGAGAFKQVLAECYNLCPEODKILV 569
Db 510 VIEPNQYFGQNGHCHKPDYQHKRDIYVLRKELGAGAFKQVLAECYNLSPFKDMGLV 569
Qy 570 AVTKLQASDNARKDFRREBELTNLDHEHVKFYGVCEGDPILMFPYMKHGLDKFL 629
Db 570 AVVALKDPITLAARDFOREBELTNLDHEHVKFYGVCGDDBPLIMFEYMKHGLDKFL 629
Qy 630 RAHGPDAVLAEGNP---PTELTSOMLHIAQOIAAGVNYLASQHFPHRDLATRNCVGS 686
Db 630 RAHGPDAVLAEGNP---PTELTSOMLHIAQOIAAGVNYLASQHFPHRDLATRNCVGS 689
Qy 687 NLVVKIDFGMSRDVSTDYR-----VGHTMLPIRMMPESIMYRKTFT 732
Db 690 NLVVKIDFGMSRDVSTDYR-----VGHTMLPIRMMPESIMYRKTFT 749
Qy 733 ESDVMSIGVNLMBIFTYGKQPYVOLSNNVEICTQORVLORPYTCQOEYELMLGCMOR 792
Db 750 ESDVMSIGVNLMBIFTYGKQPYVOLSNNVEICTQORVLORPYTCQOEYELMLGCMOR 809
Qy 793 BPHMRKNIXGHTTLQNLAKSPVYLDIG 822
Db 810 BPOORLNKIKETIKLHAGKATPYLDILG 839

RESULT 14
TRKC_CHICK STANDARD; PRT; 827 AA.
AC Q91044; Q91011; Q92022;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE NT-3 growth factor receptor precursor (BC 2.7.1.112) (TrkC tyrosine
  kinase) (Trk-C).
GN Name=TRKC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-FL, ALPHA-KT, ALPHA-KD, BETA-KD AND
  RP KI25).
RC TISSUE=Embryonic brain;
RX MEDLINE=94338700; PubMed=8060621; DOI=10.1016/0896-6273(94)90360-3;
RA Garner A.S., Large T.H.;
RT "Isoforms of the avian TrkC receptor: a novel kinase insertion

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RT dissociates transformation and process outgrowth from survival.";
RL Neuron 13:457-472(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA/FL AND TRKC-3).
RX MEDLINE=93359043; PubMed=8394830; DOI=10.1016/0014-5793(93)80216-H;
RA Okazawa H., Kamel M., Kanazawa I.;
RT "Molecular cloning and expression of a novel truncated form of chicken
  RT TrkC."
RL FEBS Lett. 329:171-177(1993).
RN [3]
RP SEQUENCE OF 378-513 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94084905; PubMed=8261614; DOI=10.1016/0165-3806(93)90028-9;
RA Williams R., Backstrom A., Ebdanal T., Hallbook F.;
RT "Molecular cloning and cellular localization of trkC in the chicken
  RT embryo."
RL Brain Res. Dev. Brain Res. 75:235-252(1993).
CC -1 FUNCTION: Receptor for neurotrophin-3 (NT-3). This is a tyrosine-
  CC protein kinase receptor. Known substrates for the trk receptors
  CC are SHC1, PI-3 kinase and PLCG1. The RT and KD isoforms fail to
  CC stimulate transformation, process outgrowth or survival. Isoform
  CC KI25 exhibits tyrosine phosphorylation in the absence of ligand
  CC and is unable to mediate survival of neuronal cells.
CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
  CC tyrosine phosphate.
CC -1 SUBUNIT: Exists in a dynamic equilibrium between monomeric (low
  CC affinity) and dimeric (high affinity) structures.
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=Alpha-FL;
CC IsoId=Q91044-1; Sequence=Displayed;
CC Name=Alpha-KT;
CC IsoId=Q91044-2; Sequence=VSP_002943; VSP_002944;
CC Name=Alpha-KD;
CC IsoId=Q91044-3; Sequence=VSP_002939; VSP_002940;
CC Name=Beta-KD;
CC IsoId=Q91044-4; Sequence=VSP_002938; VSP_002939; VSP_002940;
CC Name=TRKC-3;
CC IsoId=Q91044-5; Sequence=VSP_002941; VSP_002942;
CC Name=KI25;
CC IsoId=Q91044-6; Sequence=VSP_002945;
CC -1 DEVELOPMENTAL STAGE: Expression occurs in the embryonal day 2 (E2)
  CC embryo with increasing levels later in development. In the E9
  CC embryo highest levels are found in brain and spinal cord with
  CC intermediate levels in eye, heart, gut and muscle. Low levels are
  CC found in kidney, liver, skin and yolk sac.
CC -1 PTM: Ligand-mediated auto-phosphorylation (By similarity).
CC -1 SIMILARITY: Belongs to the tyr protein kinase family. Insulin
  CC receptor subfamily.
CC -1 SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1 SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC -1 CAUTION: The additional kinase-deleted isoform TRKC-3 which
  CC replaces the kinase domain with 19 AA instead of 39 in the isoform
  CC alpha-KD results from a frameshift.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  CC use by non-profit institutions as long as its content is in no way
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  CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
  CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; S74248; AABJ1699.1; -
DR EMBL; X59669; CAA42202.1; -
DR EMBL; Z30091; CAA82907.1; -
DR PIR; I51222; I51222.
DR PIR; I51259; I51259.
DR PIR; S35695; S35695.
DR HSBP; Q16288; IWC.
DR InterPro; IPR003599; Ig.

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Db 575 ALDPTLAARKDQFQREBELTNLOHEHIVKFGVCGGDEPLIMVFYMKHGDLNFKIFRAH 634
Cc Name=K139; Synonyms=TRKC(K139), TRKC-39;
Cc IsoId=Q03351-1; Sequence=displayed;
Cc Name=TRKC;
Cc IsoId=Q03351-2; Sequence=VSP_002936, VSP_002937;
Cc Name=K14; Synonyms=TRKC(K14), TRKC-14;
Cc IsoId=Q03351-3; Sequence=VSP_002936;
Cc Name=K125; Synonyms=TRKC-25;
Cc IsoId=Q03351-4; Sequence=VSP_002937;
Cc Name=IC158; Synonyms=TRKC(IC158), TRKCTK-;
Cc IsoId=Q03351-5; Sequence=VSP_002934, VSP_002935;
Cc Name=IC143; Synonyms=TRKC(IC143);
Cc IsoId=Q03351-6; Sequence=VSP_002932, VSP_002933;
Cc Name=IC113; Synonyms=TRKC(IC113);
Cc IsoId=Q03351-7; Sequence=VSP_002930, VSP_002931;
Cc Name=IC108; Synonyms=TRKC(IC108);
Cc IsoId=Q03351-8; Sequence=VSP_002928, VSP_002929;
Cc TISSUE SPECIFICITY: Widely expressed, mainly in the nervous
Cc tissue.
Cc -1- PTM: Ligand-mediated auto-phosphorylation.
Cc -1- SIMILARITY: Belongs to the Tyr protein kinase family. Insulin
Cc receptor subfamily.
Cc -1- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
Cc -----
Cc This SWISS-PROT entry is copyright. It is produced through a collaboration
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Cc entities requires a license agreement (See http://www.1sb-sib.ch/announce/
Cc or send an email to license@1sb-sib.ch).
Cc -----
Cc EMBL; L03813; AAA42285.1; -
Cc EMBL; L14445; AAA42282.1; -
Cc EMBL; L14446; AAA42283.1; -
Cc EMBL; L14447; AAA42284.1; -
Cc EMBL; S60953; AAB26714.2; -
Cc EMBL; S62924; AAB26716.2; -
Cc EMBL; S62933; AAB26715.2; -
Cc HSP; Q16288; IWC.
Cc RGD; 3214; Ntrk3.
Cc InterPro: IPR003599; Ig.
Cc InterPro: IPR007110; Ig-like.
Cc InterPro: IPR011009; Kinase_like.
Cc InterPro: IPR001611; LRR.
Cc InterPro: IPR000483; LRR_Cterm.
Cc InterPro: IPR000372; LRR_Nterm.
Cc InterPro: IPR002011; ReceptCytkinait.
Cc InterPro: IPR001245; Tyr_kinase.
Cc InterPro: IPR008266; Tyr_pkinase_AS.
Cc Pfam; PF00047; Ig_1.
Cc Pfam; PF00560; LRR_2.
Cc Pfam; PF01462; LRRNT_1.
Cc Pfam; PF00069; Kinase_1.
Cc PRINTS; PR00019; LRRICHRPT.
Cc PRODOM; PD000001; Prok_kinase_1.
Cc SMART; SM00409; Ig_1.
Cc SMART; SM00082; LRRCT_1.
Cc SMART; SM00013; LRRNT_1.
Cc SMART; SM00219; Tyrc; 1.
Cc PROSITE; PS50835; IG LIKE_1.
Cc PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
Cc PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
Cc PROSITE; PS00109; PROTEIN_KINASE_TYR_1.
Cc PROSITE; PS00239; RECEPTOR_TYR_KIN_II_1.
Cc Alternative splicing; ATP-Binding; Glycoprotein;
Cc Immunoglobulin domain; Leucine-rich repeat; Neurogenesis;
Cc Phosphorylation; Receptor; Repeat; Signal; Transferrase; Transmembrane;
Cc Tyrosine-protein kinase.
Cc SIGNAL 1 31 By similarity.
Cc CHAIN 1 864 NT-3 growth factor receptor.
Cc FT

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FT DOMAIN 32 429 Extracellular (Potential).
FT TRANSMEM 430 453 Potential.
FT DOMAIN 454 864 Cytoplasmic (Potential).
FT REPEAT 102 125 LRR 1.
FT REPEAT 126 149 LRR 2.
FT DOMAIN 210 300 Ig-like C2-type 1.
FT DOMAIN 309 382 Ig-like C2-type 2.
FT DOMAIN 538 853 Protein kinase.
FT NP BIND 544 552 ATP (By similarity).
FT BINDING 572 572 ATP (By similarity).
FT ACT SITE 679 679 Proton acceptor (By similarity).
FT MOD_RES 516 516 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 705 705 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 709 709 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 710 710 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 859 859 Phosphotyrosine (by autocatalysis) (By similarity).
FT SITE 516 516 Interaction with SHC1 (By similarity).
FT SITE 859 859 Interaction with PLC-gamma-1 (By similarity).
FT CARBOHYD 68 68 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 72 72 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 79 79 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 163 163 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 203 203 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 232 232 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 267 267 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 272 272 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 375 375 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 388 388 N-linked (GlcNAc... ) (Potential).
FT VARSPLIC 529 562 YVOHKKRDYTLKRELGEAGFGKVFLEACYNLSPTKDKM
IEGFAVGRVYVMTSVHCHPCWFRFGLEML (in isoform IC108).
FT VARSPLIC 563 864 /FtId=VSP_002928.
Missing (in isoform IC108).
FT VARSPLIC 529 567 /FtId=VSP_002929.
YVOHKKRDYTLKRELGEAGFGKVFLEACYNLSPTKDKM
-> CFEKIMNPISLSGHSKPLNNGIYEDVNVYFSKGRHG
F (in isoform IC113).
FT VARSPLIC 568 864 /FtId=VSP_002930.
Missing (in isoform IC113).
FT VARSPLIC 529 597 /FtId=VSP_002931.
YVOHKKRDYTLKRELGEAGFGKVFLEACYNLSPTKDKM
AVKALKDPTLAKRDFORBAELTNLQHEHIVKRYGCGDG
DP -> WFSNIDNHGILNKNRNDHVLVPSHTYIEBPVQ
GILNKNRNDHVLVPSHTYIEBPVQSGDVSPSHGELLP
LTSLEYEVKPLPLVLIKT (in isoform IC143).
FT VARSPLIC 598 864 /FtId=VSP_002933.
Missing (in isoform IC143).
FT VARSPLIC 529 612 /FtId=VSP_002934.
YVOHKKRDYTLKRELGEAGFGKVFLEACYNLSPTKDKM
AVKALKDPTLAKRDFORBAELTNLQHEHIVKRYGCGDG
DP -> WFSNIDNHGILNKNRNDHVLVPSHTYIEBPVQ
GILNKNRNDHVLVPSHTYIEBPVQSGDVSPSHGELLP
LTSLEYEVKPLPLVLIKT (in isoform IC158).
FT VARSPLIC 613 864 /FtId=VSP_002936.
Missing (in isoform IC158).
FT VARSPLIC 712 736 /FtId=VSP_002935.
Missing (in isoform K14 and isoform TRK).
FT VARSPLIC 737 750 /FtId=VSP_002937.
Missing (in isoform K125 and isoform TRK).
SQ SEQUENCE 864 AA; 97063 MW; A202B93E208F636 CRC64;

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Query Match 51.3%; Score 2266.5; DB 1; Length 864;
Best Local Similarity 52.6%; Pred. No. 1,le-124;
Matches 468; Conservative 107; Mismatches 206; Indels 109; Gaps 17;

Qy 10 PAMARLW-----GFCWL-VVGFWRARACPTSCCKSARIMCSPBSPGIAFPPLP--- 60
Db 7 PACSEFWRITLDSVWLDVVG---SVLACPANCVCSTETINCRPPDGNL-FPLLEQDS 62

Qy 61 -----NSVD-PENITETIFIANQKLEIINEDVEAVYGLNLTIVDSGLKFAVHAKA 110
Db 63 GNSNGASNIITDISKRITSIHLENRGHTLANVAMELYTGLQKLTIRNSGLRNIPRA 122

Qy 111 FLANSNLQHINFRANKLTLSRRKFRHLDSLEILVGNPFTGSCDIMIKTLQF-AKSSP 169
Db 123 FAKNPILRYINLSSNRLLTTLSSWQLFQTLSSRELBEQNFNCSGDIIMQMLQEGEARL 182

Qy 170 DTQDLYLANSSKNIPLANIQINCGLPANLAAPNLTVEEGSITLTSVAGPVRNMY 229
Db 183 DSQSLYCISADGSQLPFRNNISQCDLPEISVSHVNLTVREBDNAVITCNSSGSLPDPVD 242

Qy 230 MDVGNLVS-----KHMETSHTQSLRITNYSDDSGKOISCVANLVGEODSDVNTLVH 284
Db 243 WITPGLQSIINTHOTNLTMTVVAINTLVNTSEDNFTLTCLANVGNASNSALVTY 302

Qy 285 PAPTTFLESPTSDHHCIPFTYKGNPKPALQWFPYNGALINESKYICTKJHVTNHTYH- 343
Db 303 YPRPVSVLVEPEVRLHEICIEFVVRGNPTPLHMLYNGQPLRESKII-----HMDYQ 354

Qy 344 -----GCLQDLPFTKNNEDYTLIANEYGEKQKQISAFPMGPGIDGANPYPDYIY 397
Db 355 EGEVSECCLEFNKPTHTNNGNYTLIANALGTANQTINGHFLEKPP-----FPE--- 402

Qy 398 EDVGTANDIGDTNRENEIPSTDVDTKGREHLSYAAVVIVASVGFCL-LVWLFL-- 454
Db 403 -----STDFPDESASPTPTTYTHKPEEDTFGSIANGLAFA--CVLLVLFMTIN 454

Qy 455 KLAHRSFKGKGPASVISNDSDASPLMHSNGSNTPSSBGGDAVIIGTKIPIVENP 514
Db 455 KYGRBSRFKMGKPAVAIVSGEDSASPLMHNHIGITPSSLDAGPDVTIVGTRIPVLENP 514

Qy 515 QYFGITNSQLKPTDTPVQHIGRHNIVLKRLEGEAGFGKVFLEACYNLCPEDQKILVAVKTL 574
Db 515 QYRQGNCHCKPPTYVOHKKRDYTLKRELGEAGFGKVFLEACYNLSPTKDKMLVAVKAL 574

Qy 575 KDSADNARKDFHREBELTNLQHEHIVKRYGCVGEGDPLIMVEPYMGRGDKNKLRAHGP 634
Db 575 KDPTLAKRDFORBAELTNLQHEHIVKRYGCVGEGDPLIMVEPYMGRGDKNKLRAHGP 634

Qy 635 DAVLMAEGNP---PTELTOGQMLHIAQOIAAGVYLLASQHFVHRDLATRNCLVGENLLVK 691
Db 635 DAMILVDGQROAKGELGSLQMLHIASQIASGVYLLASQHFVHRDLATRNCLVGENLLVK 694

Qy 692 IGDGMSRDVYSTDYR-----VGGH 712
Db 695 IGDGMSRDVYSTDYREBPYQKGFPSVSWQOORLAASAATLFPNPGNDFCIWCEVGH 754

Qy 713 TMLPIRMPRESIMYRPTTESDVMSLGVLTMLFTYGGKQPVQOLSNMYIECTOORVL 772
Db 755 TMLPIRMPRESIMYRPTTESDVMSFGVILMELFTYGGKQPVQOLSNMYIECTOORVL 814

Qy 773 QRPRTCPOEYVBLMGCMQREPHRKNIKIHITLQNLALASAPYLDILG 822
Db 815 ERRRVCKEYVDVMLGCMQREPOORLNKIYKILHLAGRATPYLDILG 864

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Search completed: February 17, 2005, 00:27:28  
 Job time : 183 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 17, 2005, 00:18:38 ; Search time 45 Seconds  
(without alignments)

1757,560 Million cell updates/sec

Title: US-10-645-546-2

Perfect score: 4419

Sequence: 1 MSSWIRWHPGPMARLMGFCW.....ITLLQNLAKASPYVLDILG 822

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4419	100.0	822	1 A56853	brain-derived neur
2	4179.5	94.6	821	1 S06943	brain-derived neur
3	4162.5	94.2	821	1 A39667	brain-derived neur
4	3426	77.5	818	1 S44098	brain-derived neur
5	2520	57.0	477	1 I73631	brain-derived neur
6	2292.5	51.9	476	1 A35104	brain-derived neur
7	2289	51.8	825	2 A55178	neurotrophin-3 recep
8	2277	51.5	839	1 I73632	neurotrophin-3 recep
9	2275.5	51.5	474	1 C39667	brain-derived neur
10	2275.5	51.5	476	1 B39667	brain-derived neur
11	2252.5	51.0	852	2 I51259	tyrosine kinase C
12	2178	49.3	825	1 A40026	neurotrophin-3 recep
13	2149.5	48.6	803	1 S35695	neurotrophin-3 recep
14	1901	43.0	799	1 TVRUTB	nerve growth facto
15	1893.5	42.8	790	1 TVRUTB	nerve growth facto
16	1564	35.4	520	1 S44099	brain-derived neur
17	1420.5	32.1	282	2 I51236	brain-derived neur
18	1249	28.3	503	4 S21741	hypothetical TRP/T
19	989	22.4	612	2 I73633	gene trkC protein
20	856	19.4	871	2 I48696	protein-tyrosine k
21	856	19.4	881	1 A48697	protein-tyrosine k
22	850	19.2	525	1 A58674	neurotrophin-3 recep
23	798	18.1	945	1 A47299	ror-related recep
24	749	16.9	685	1 A48289	neurotrophic recep
25	722	16.3	937	2 A45082	neurotrophic recep
26	703.5	15.9	943	2 B45082	tyro 10 receptor k
27	685.5	15.5	819	2 I48859	insulin-like growth
28	679.5	15.4	1367	1 IGHUR1	kinase-like protei
29	676.5	15.3	1051	2 A39712	

30	676	15.3	806	2 A35963	protein-tyrosine k
31	676	15.3	855	2 A42621	nerve growth facto
32	674	15.2	168	2 I51297	heparin-binding gr
33	673.5	15.2	1371	2 A31837	heparin-binding gr
34	672.5	15.2	800	2 A48991	insulin-like growth
35	671.5	15.2	797	2 S38579	insulin-like growth
36	670.5	15.2	640	2 S23008	insulin-like growth
37	669.5	15.2	800	1 TVH02F	fibroblast growth
38	661	15.0	801	2 I55363	fibroblast growth
39	658	14.9	876	2 A49508	tyrosine kinase k
40	656	14.8	910	2 A53137	tyrosine kinase re
41	655	14.8	913	2 A48280	receptor tyrosine
42	654	14.8	806	1 TVH0D3	fibroblast growth
43	652.5	14.8	1070	2 JC4593	protein-tyrosine k
44	642	14.5	1363	2 T43220	insulin-like growth
45	640.5	14.5	819	1 TVCHFG	fibroblast growth

## ALIGNMENTS

## RESULT 1

A56853 brain-derived neurotrophic factor receptor precursor - human

N/Alternate names: receptor tyrosine kinase trkB

C/Contains: protein-tyrosine kinase (EC 2.7.1.112)

C/Species: Homo sapiens (man)

C/Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 09-Jul-2004

C/Accession: A56853; I56557

R/Nakagawara, A.; Lin, X.G.; Ikegaki, N.; White, P.S.; Yamashiro, D.J.; Nycum, L.M.; Bie

Genomic 25, 538-546, 1995

A/Title: Cloning and chromosomal localization of the human TRK-B tyrosine kinase recepto

A/Reference number: A56853; MUID:95309922; PMID:7789988

A/Molecule type: mRNA

A/Residues: 1-822 <SHR>

A/Cross-references: GB:576473; NID:913717; PIDN:AAB33109.1; PID:913718

C/Genetics: A:Gene: GDB:NTRK2; trkB

A/Cross-references: GDB:127898; OMIM:600456

A/Map position: 9q22.1-9q22.1

C/Function: A:Description: regulation of nervous system development; receptor for brain-derived neur

C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr

C/Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor ;

inase

F.1-31/Domain: signal sequence #status predicted <SIG>

F.32-822/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>

F.32-433/Domain: extracellular #status predicted <EXT>

F.67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F.92-118/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F.113-118/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F.139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR

F.436-452/Domain: transmembrane #status predicted <TM>

F.453-822/Domain: cytosolic #status predicted <CYT>

F.536-814/Domain: protein kinase homology <KIN>

F.544-552/Region: protein kinase ATP-binding motif

F.567-95/Region: 121,178,205,241,254,280,325,338,350,412/Binding site: carbohydrate (Aan) (covalen

F.572/Active site: lys #status predicted

F.706/Binding site: phosphate (Tyr) (covalent) #status predicted

F.817/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 4419; DB 1; Length 822;

Best Local Similarity 100.0%; Pred. No. 9e-204;

Matches	822:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
Qy	1	MSWIRHNGPAMALWGF	CMLVGF	WRAAFACPTSCCKSASRIWCDSPSGIVAFPLLEP	60				
Db	1	MSWIRHNGPAMALWGF	CMLVGF	WRAAFACPTSCCKSASRIWCDSPSGIVAFPLLEP	60				
Qy	61	NSVDPENITEFIANOKRL	EINBDDVEAYVGL	ENLITVDSGLKFAVAAKFLKNSNIQHI	120				
Db	61	NSVDPENITEFIANOKRL	EINBDDVEAYVGL	ENLITVDSGLKFAVAAKFLKNSNIQHI	120				
Qy	121	NFRNKLTSLSRKHFRHLD	ISELLVGNPFTCS	CDIMWIKTLQRAKSSPTQDLYCLNES	180				
Db	121	NFRNKLTSLSRKHFRHLD	ISELLVGNPFTCS	CDIMWIKTLQRAKSSPTQDLYCLNES	180				
Qy	181	SKNPLANLQIPNCGSP	ANLAAPNLTV	BEKSGITLSCSVAGDPVPMYMDVGNLVSKM	240				
Db	181	SKNPLANLQIPNCGSP	ANLAAPNLTV	BEKSGITLSCSVAGDPVPMYMDVGNLVSKM	240				
Qy	241	NETSHTQGSRLITNIS	SDSGKOISCAVENLV	GEDDSVNLTVHFAPTITFLSPSDHH	300				
Db	241	NETSHTQGSRLITNIS	SDSGKOISCAVENLV	GEDDSVNLTVHFAPTITFLSPSDHH	300				
Qy	301	WCIPFTVKGNP	KPALQWFYNGAL	INESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT	360				
Db	301	WCIPFTVKGNP	KPALQWFYNGAL	INESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT	360				
Qy	361	LIANRYGKDEKQISAH	FWMGPGIDGAPNY	PDVIYEDYGTANDIGDTTNSNRIPIST	420				
Db	361	LIANRYGKDEKQISAH	FWMGPGIDGAPNY	PDVIYEDYGTANDIGDTTNSNRIPIST	420				
Qy	421	DVDTKTRGRLSHVAA	VVVVIVSVGFCL	VMLFLKLARHSGFKMGKSPASVYSNDDDSASP	480				
Db	421	DVDTKTRGRLSHVAA	VVVVIVSVGFCL	VMLFLKLARHSGFKMGKSPASVYSNDDDSASP	480				
Qy	481	LHHISNGSNTSSSEGG	PDVAIIIGMTKIP	VIENPOYFGITNSQKPDPTFOHIKRHNIYL	540				
Db	481	LHHISNGSNTSSSEGG	PDVAIIIGMTKIP	VIENPOYFGITNSQKPDPTFOHIKRHNIYL	540				
Qy	541	KRELGEAGFGKVF	LAECYNLCPEODKIL	VAVKTLKQASDNARKDFAHEABLLTNLOHEHI	600				
Db	541	KRELGEAGFGKVF	LAECYNLCPEODKIL	VAVKTLKQASDNARKDFAHEABLLTNLOHEHI	600				
Qy	601	VKPYGVCVEBDPL	IMVEFYMGKGLNK	FLRAHSGDAVLAEGNPPTTELTOGOMLHIAQOI	660				
Db	601	VKPYGVCVEBDPL	IMVEFYMGKGLNK	FLRAHSGDAVLAEGNPPTTELTOGOMLHIAQOI	660				
Qy	661	AAGWVYLASQHF	VRDLATRNCLV	GENLVKIGDFGMSRDVYSTDYRYVGHTMLPIRMM	720				
Db	661	AAGWVYLASQHF	VRDLATRNCLV	GENLVKIGDFGMSRDVYSTDYRYVGHTMLPIRMM	720				
Qy	721	PPESIMYRKFTTS	DVMSLGVLM	EFTYQKQPMYQLSNNEVEICITOGVLOPRTCPQ	780				
Db	721	PPESIMYRKFTTS	DVMSLGVLM	EFTYQKQPMYQLSNNEVEICITOGVLOPRTCPQ	780				
Qy	781	EVEYELMLGCMQ	REPHMKNIKGI	HTLLONLAKASPVYLDIIG	822				
Db	781	EVEYELMLGCMQ	REPHMKNIKGI	HTLLONLAKASPVYLDIIG	822				

## RESULT 2

506943  
brain-derived neurotrophic factor receptor precursor - mouse  
N:Alternate names: receptor tyrosine kinase trkB  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: S06943  
R:Klein, R.; Parada, L.F.; Coulier, F.; Barbacid, M.  
EMBO J. 8, 3701-3709, 1989  
A:Title: trkB, a novel tyrosine protein kinase receptor expressed during mouse neural de  
A:Reference number: S06943; MUID:9005970; PMID:2555172  
A:Accession: S06943  
A:Molecule type: mRNA

A:Residues: 1-821 <trkB>					
A:Cross-references: UNIPROT:P15209; EMBL:X17647; NID:955505; PIDN:CAA53636.1; PID:955506					
C:Genetics:					
A:Gene: trkB					
C:Function:					
A:Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor					
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein					
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor 1					
inaae					
F:1-31/Domain: signal sequence #status predicted <SIG>					
F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>					
F:32-434/Domain: extracellular #status predicted <EXT>					
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>					
F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>					
F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>					
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR4>					
F:145-451/Domain: transmembrane #status predicted <CYT>					
F:452-821/Domain: cytosolic #status predicted <CYT>					
F:535-813/Domain: protein kinase homology <KIN>					
F:543-551/Region: protein kinase ATP-binding motif					
F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Asn) (covalent)					
F:571/Active site: Lys #status predicted					
F:706/Binding site: phosphate (Tyr) (covalent) #status predicted					
F:816/Binding site: phosphate (Tyr) (covalent) #status predicted					
Query Match	94.6%; Score 4179.5; DB 1; Length 821;				
Best Local Similarity	93.9%; Pred. No. 2,4e-192;				
Matches	772; Conservative 27; Mismatches 22; Indels 1; Gaps 1;				
Qy	1	MSWIRHNGPAMALWGF	CMLVGF	WRAAFACPTSCCKSASRIWCDSPSGIVAFPLLEP	60
Db	1	MSWIRHNGPAMALWGF	CMLVGF	WRAAFACPTSCCKSASRIWCDSPSGIVAFPLLEP	60
Qy	61	NSVDPENITEFIANOKRL	EINBDDVEAYVGL	ENLITVDSGLKFAVAAKFLKNSNIQHI	120
Db	61	NSVDPENITEFIANOKRL	EINBDDVEAYVGL	ENLITVDSGLKFAVAAKFLKNSNIQHI	120
Qy	121	NFRNKLTSLSRKHFRHLD	ISELLVGNPFTCS	CDIMWIKTLQRAKSSPTQDLYCLNES	180
Db	121	NFRNKLTSLSRKHFRHLD	ISELLVGNPFTCS	CDIMWIKTLQRAKSSPTQDLYCLNES	180
Qy	181	SKNPLANLQIPNCGSP	ANLAAPNLTV	BEKSGITLSCSVAGDPVPMYMDVGNLVSKM	240
Db	181	SKNPLANLQIPNCGSP	ANLAAPNLTV	BEKSGITLSCSVAGDPVPMYMDVGNLVSKM	240
Qy	241	NETSHTQGSRLITNIS	SDSGKOISCAVENLV	GEDDSVNLTVHFAPTITFLSPSDHH	300
Db	241	NETSHTQGSRLITNIS	SDSGKOISCAVENLV	GEDDSVNLTVHFAPTITFLSPSDHH	300
Qy	301	WCIPFTVKGNP	KPALQWFYNGAL	INESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT	360
Db	301	WCIPFTVKGNP	KPALQWFYNGAL	INESKYICTKIHTNHTHYGCLQLDNPTMANNQDYT	360
Qy	361	LIANRYGKDEKQISAH	FWMGPGIDGAPNY	PDVIYEDYGTANDIGDTTNSNRIPIST	420
Db	361	LIANRYGKDEKQISAH	FWMGPGIDGAPNY	PDVIYEDYGTANDIGDTTNSNRIPIST	420
Qy	421	DVDTKTRGRLSHVAA	VVVVIVSVGFCL	VMLFLKLARHSGFKMGKSPASVYSNDDDSASP	480
Db	421	DVDTKTRGRLSHVAA	VVVVIVSVGFCL	VMLFLKLARHSGFKMGKSPASVYSNDDDSASP	480
Qy	481	LHHISNGSNTSSSEGG	PDVAIIIGMTKIP	VIENPOYFGITNSQKPDPTFOHIKRHNIYL	540
Db	481	LHHISNGSNTSSSEGG	PDVAIIIGMTKIP	VIENPOYFGITNSQKPDPTFOHIKRHNIYL	540
Qy	541	KRELGEAGFGKVF	LAECYNLCPEODKIL	VAVKTLKQASDNARKDFAHEABLLTNLOHEHI	600
Db	541	KRELGEAGFGKVF	LAECYNLCPEODKIL	VAVKTLKQASDNARKDFAHEABLLTNLOHEHI	600
Qy	601	VKPYGVCVEBDPL	IMVEFYMGKGLNK	FLRAHSGDAVLAEGNPPTTELTOGOMLHIAQOI	660
Db	601	VKPYGVCVEBDPL	IMVEFYMGKGLNK	FLRAHSGDAVLAEGNPPTTELTOGOMLHIAQOI	660



Qy 661 AAGVYIASOHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 720  
 Db 660 AAGVYIASOHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 719  
 Qy 721 PPSIMYRKFTTSDVMSLGVLMELFTYGKOPWQLSNNEVEICTIQGRVLOPRPCQ 780  
 Db 720 PPSIMYRKFTTSDVMSLGVLMELFTYGKOPWQLSNNEVEICTIQGRVLOPRPCQ 779  
 Qy 781 EYVELMIGCQORBPBRKNIKIGHTLLQNLAKASPVYLDILG 822  
 Db 780 EYVELMIGCQORBPBRKNIKIGHTLLQNLAKASPVYLDILG 821

## RESULT 3

A39667  
 brain-derived neurotrophic factor receptor precursor - rat  
 N:Alternate names: receptor tyrosine kinase trkB.FL  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 09-Jul-2004  
 C:Accession: A39667  
 R:Middleman, D.S.; Lindberg, R.A.; Hunter, T.  
 Mol. Cell. Biol. 11, 143-153, 1991  
 A:Title: trkB, a neural receptor protein-tyrosine kinase: evidence for a full-length and  
 A:Reference number: A39667; MUID:91094826; PMID:1846020  
 A:Accession: A39667  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-821 <MID>  
 A:Cross-references: UNIPROT:Q63604; GB:M55291; NID:9207473; PID:AAA42279.1; PID:9207474  
 C:Function:  
 A:Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein  
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor kinase  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>  
 F:32-434/Domain: extracellular #status predicted <EXT>  
 F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
 F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
 F:435-451/Domain: transmembrane #status predicted <TM>  
 F:452-821/Domain: cytosolic #status predicted <CYT>  
 F:553-813/Domain: protein kinase homology <KIN>  
 F:553-551/Region: protein kinase ATP-binding motif  
 F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carboxylate (Asn) (covalent)  
 F:571/Active site: Lys #status predicted  
 F:705/Binding site: phosphate (Tyr) (covalent) #status predicted  
 F:816/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 94.2%; Score 4162.5; DB 1; Length 821;  
 Best Local Similarity 93.6%; Pred. No. 1.6e-191;  
 Matches 769; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MSSYIRHNGPMARLVGFCMLVGFMAAPFPTSCSCASRIKICSPSPGIVAFPRHP 60  
 Db 1 MSSYIRHNGPMARLVGFCMLVGFMAAPFPTSCSCASRIKICSPSPGIVAFPRHP 60  
 Qy 61 NSVDPENITELIFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVAKAFKSNLQHI 120  
 Db 61 NSVDPENITELIFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVAKAFKSNLQHI 120  
 Qy 121 NPTNKTLSLRKAFRHLDELIVGNPFTSCDIDIMKIKLOAKSPDQDYCLANES 180  
 Db 121 NPTNKTLSLRKAFRHLDELIVGNPFTSCDIDIMKIKLOAKSPDQDYCLANES 180  
 Qy 121 NPTNKTLSLRKAFRHLDELIVGNPFTSCDIDIMKIKLOAKSPDQDYCLANES 180  
 Db 121 NPTNKTLSLRKAFRHLDELIVGNPFTSCDIDIMKIKLOAKSPDQDYCLANES 180  
 Qy 181 SKNPLANLQIPNGCLPSARLAAPNLTYEBSKSTISSVSGDDPLPIIYMGVNLVSKM 240  
 Db 181 SKNPLANLQIPNGCLPSARLAAPNLTYEBSKSTISSVSGDDPLPIIYMGVNLVSKM 240  
 Qy 241 NETSHTOGLRITNISDDSGKOISCAVNLVGEDDQSVNLTVHAPPTITLESPTSDDH 300  
 Db 241 NETSHTOGLRITNISDDSGKOISCAVNLVGEDDQSVNLTVHAPPTITLESPTSDDH 300

Db 241 NETSHTOGLRITNISDDSGKOISCAVNLVGEDDQSVNLTVHAPPTITLESPTSDDH 300  
 Qy 301 WCIPTFVKNPKPALQMFVNGALINBSKYICTKIHVTNHTYHGLQLDNPTMANNQDY 360  
 Db 301 WCIPTFVKNPKPALQMFVNGALINBSKYICTKIHVTNHTYHGLQLDNPTMANNQDY 360  
 Qy 361 LIANKEYGKDEKQISAHFMWPGIDGANDPNVYEDYGYANDIGDTTNSNEIPST 420  
 Db 361 LIANKEYGKDEKQISAHFMWPGIDGANDPNVYEDYGYANDIGDTTNSNEIPST 419  
 Qy 421 DVTDKTGREHLSYAAVAVVAVSVGFCLVNLPLILKLARHSGKPGASVTSNDSDASP 480  
 Db 420 DVADQTNREHLSYAAVAVVAVSVGFCLVNLPLILKLARHSGKPGASVTSNDSDASP 479  
 Qy 481 LHHISNGSNTPSSSEGGPDVVIIGMTKIPITENPOYEGITNSOLKPTFOHIKRHVYL 540  
 Db 480 LHHISNGSNTPSSSEGGPDVVIIGMTKIPITENPOYEGITNSOLKPTFOHIKRHVYL 539  
 Qy 541 KRELGEAGFGKVFLEACVNLCPRODKILVAVKTLKQASDNARKDFHREBELTNLOHEHI 600  
 Db 540 KRELGEAGFGKVFLEACVNLCPRODKILVAVKTLKQASDNARKDFHREBELTNLOHEHI 599  
 Qy 601 VKTYGVCEGDPILMVEYKMGDLNKFLEAHGPDVLAEGNPPTLTOSQMLHIAQOI 660  
 Db 600 VKTYGVCEGDPILMVEYKMGDLNKFLEAHGPDVLAEGNPPTLTOSQMLHIAQOI 659  
 Qy 661 AAGVYIASOHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 720  
 Db 660 AAGVYIASOHFVHRDLATNCLVGENLVLKIGDFGMSRDVYSTDYRVGCHTMLPIRMM 719  
 Qy 721 PPSIMYRKFTTSDVMSLGVLMELFTYGKOPWQLSNNEVEICTIQGRVLOPRPCQ 780  
 Db 720 PPSIMYRKFTTSDVMSLGVLMELFTYGKOPWQLSNNEVEICTIQGRVLOPRPCQ 779  
 Qy 781 EYVELMIGCQORBPBRKNIKIGHTLLQNLAKASPVYLDILG 822  
 Db 780 EYVELMIGCQORBPBRKNIKIGHTLLQNLAKASPVYLDILG 821

## RESULT 4

brain-derived neurotrophic factor receptor precursor - chicken  
 N:Alternate names: receptor tyrosine kinase trkB  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S59399; S42175; S44098  
 R:Vin, N.O.; Erdmann, K.S.; Heumann, R.  
 Gene 149, 383-384, 1994  
 A:Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of the  
 A:Reference number: S59398; MUID:95047511; PMID:7959025  
 A:Accession: S59399  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-818 <VI2>  
 A:Cross-references: UNIPROT:Q91987; EMBL:X77251; NID:9563881; PID:CAA54468.1; PID:94729  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994  
 R:Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Potgiesser, J.; Berde, Y.A.  
 Development 119, 545-558, 1993  
 A:Title: Expression and binding characteristics of the BDNF receptor chick trkB.  
 A:Reference number: S42175; MUID:94116452; PMID:8287802  
 A:Accession: S42175  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-818 <DEC>  
 A:Cross-references: EMBL:X74109; NID:9407798; PID:CAA52210.1; PID:9407799  
 C:Gene: trkB  
 C:Function:  
 A:Description: regulation of nervous system development; receptor for brain-derived neurotrophic factor  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein  
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor kinase

F:1-31/Domain: signal sequence #status predicted <SIG>  
F:32-818/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>  
F:32-432/Domain: extracellular #status predicted <EXT>  
F:65-90/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:115-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:138-149/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR4>  
F:433-449/Domain: transmembrane #status predicted <TM>  
F:450-818/Domain: cytosolic #status predicted <CYT>  
F:532-810/Domain: protein kinase homology <KIN>  
F:540-548/Region: protein kinase ATP-binding motif  
F:66-94,120,139,204,253,287,324,337,349,408/Binding site: carbohydrate (Aan) (covalent)  
F:568/Active site: lys #status predicted  
F:702/Binding site: phosphate (Tyr) (covalent) #status predicted  
F:813/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 77.5%; Score 3426; DB 1; Length 818;  
Best Local Similarity 77.6%; Pred. No. 2,2e-156;  
Matches 638; Conservative 73; Mismatches 107; Indels 4; Gaps 3;

QY 1 MSSWIRHGPAMARLWGFVWFWRAAFACPTSCSCASRIWCSDPSPGIYAFPLRP 60  
DB 1 MWSRRRPGPLARLWGLVGCWFGALGCPASCRSSWRICSPVIGITSFF-VPG 59  
QY 61 NSVDPENITFIYANOKRELIINDDVAYVGLRNLTIVDSGLKFVAHKAFLKNSNQHI 120  
DB 60 RSTDDVNTETIYANOKRELIINDDVAYVGLRNLTIVDSGLKFVAHKAFLKNSNQHI 119  
QY 121 NFRNKLTSLSRKHFRHLDSELIIVGNPFTCSCDIMWIKTLQBAKSSPTDOLYCLNES 180  
DB 120 NLSNKLSSSKKFRHLDSELIIVGNPFTCSCEIMWIKFRQTKYTEQDLYCVDN 179  
QY 181 SKNIPLANLOIPNCGLPANLAANLTVEEGKSTITLSCVAGDPVPMYVDGNLVSKM 240  
DB 180 NKRIALMDKVPNCDLPSANLSNNTIVYEGSKITIVCDTTCGPPVSWLTNLVSNHE 239  
QY 241 NETHTGOSLRITITSSDDSKQISCAVENIVGEDQDSVNLTHFAPTTFLESPTSDH 300  
DB 240 SDTSKPNASLTITKNVSSDGLWISCAVENIVGQTSABLTVPFAPNITFIESPTDDH 299  
QY 301 WCIPFTYKGNPKPALOWFYNGAILNESKYCTCKHNTNHTYHGCLOLDNTHANNQDY 360  
DB 300 WCIPFTYKGNPKPALOWFYNGAILNESKYCTCKHNTNHTYHGCLOLDNTHANNQDY 359  
QY 361 LIANRYGDKBEKQISAHPWMPGIDGAPNYPVIVEDYEDYGTANDIGDTTNSNEIPST 420  
DB 360 LIANRYGDKBEKQISAHPWMPGIDGAPNYPVIVEDYEDYGTANDIGDTTNSNEIPST 416  
QY 421 DVTDKTGRBHLVYAVVVIASVGFCLVWLFLIKLARHSKFGKGPASVISNDSDASP 480  
DB 417 DVSNKERNEDSTIVVVVVGIAALVCTGLVIMLILKFGHSHKFGMKGPSVISNDSDASP 476  
QY 481 LHHNSGNSPTSSSEGGPDVYIIMTKIPVIEENPOYGIINSOLKPTPOHITRHHIVL 540  
DB 477 LHHNSGNSPTSSSEGGPDVYIIMTKIPVIEENPOYGIINSOLKPTPOHITRHHIVL 536  
QY 541 KRREIGGAFGVAFABCYNLCPEDDKILVAVKTLKASDANRKPFRHEAELLTLVQHEHI 600  
DB 537 KRREIGGAFGVAFABCYNLCPEDDKILVAVKTLKASDANRKPFRHEAELLTLVQHEHI 596  
QY 601 VKPYGVCVEGDPILMVEFYMGHGLNKLRAHGPDAVLAEGNPTELTOGMLHIAQOI 660  
DB 597 VKPYGVCVEGDPILMVEFYMGHGLNKLRAHGPDAVLAEGNPTELTOGMLHIAQOI 656  
QY 661 AAGNVYLASOHFVRDLATRNCLVGENLTVKIGDPGMSRDVSTDYRVRGHTMLPIRMM 720  
DB 657 AAGNVYLASOHFVRDLATRNCLVGENLTVKIGDPGMSRDVSTDYRVRGHTMLPIRMM 716  
QY 721 PPSIMTRKFTTSDVMSIGVVLWEIFTYQKPYOLSNNEVICITQGRVLOSPRTCPQ 780  
DB 717 PPSIMTRKFTTSDVMSIGVVLWEIFTYQKPYOLSNNEVICITQGRVLOSPRTCPQ 776  
QY 781 EYVEIMLGCWQREPHMRKNIGIHTLONLAKASPVYLDLIG 822

DB 777 EYVDLMLGCWQREPHMRKNILKEIHSILONLAKASPVYLDLIG 818

## RESULT 5

173631

brain-derived neurotrophic factor receptor precursor, short splice form - human

N/Alternate names: neurotrophin receptor trkB; truncated receptor tyrosine kinase trkB

C/Species: Homo sapiens (man)

C/Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text\_change 09-Jul-2004

C/Accession: 173631; 138357; 566384; 544129

R/Shelton, D.L.; Suberland, J.; Griep, U.; Camerotto, T.; Aramant, M.P.; Phillips, H.S.;

J. Neurosci. 15, 477-491, 1995

A>Title: Human trks: molecular cloning, tissue distribution, and expression of extracell

A/Reference number: 156557; PMID:95123473; PMID:7823356

A/Accession: 173631

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-477 &lt;RES&gt;

A/Cross-references: UNIPROT:Q16620; GB:S76474; NID:913719; PID:AA33110.1; PID:g913720

R/Allen, S.J.; Dawbarn, D.; Eckford, S.D.; Wilcock, G.K.; Ashcroft, M.; Colebrook, S.M.;

Neuroscience 60, 825-834, 1994

A>Title: Cloning of a non-catalytic form of human trkB and distribution of messenger RNA

A/Reference number: 138357; PMID:95022162; PMID:7936202

A/Accession: 138357

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-477 &lt;RES&gt;

A/Cross-references: NID:9473007; PID:CA53571.1; PID:9473008

R/Henly, M.; Talyemimo, T.; Le, J.; Katta, V.; Welcher, A.; Rohde, M.F.

Arch. Biochem. Biophys. 322, 256-264, 1995

A>Title: Extracellular domain of neurotrophin receptor trkB: disulfide structure, N-glyc

A/Reference number: 566384; PMID:96004804; PMID:7574684

A/Accession: 566384

A/Molecule type: protein

A/Residues: 33-3738-42,43-57,143-155,167-179,183-199,302-308,329-333,334-337,'X',339-346

C/Comment: This form of the receptor is missing the protein kinase domain.

C/Genes: GDB:NTRK2; trkB

A/Cross-references: GDB:127898; OMIM:600456

A/Map position: 9q22.1-9q22.1

C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop

C/Keyword: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; C

F:1-31/Domain: signal sequence #status predicted &lt;SIG&gt;

F:32-477/Product: brain-derived neurotrophic factor receptor, short splice form #status I

F:32-435/Domain: extracellular #status predicted &lt;EXT&gt;

F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR2&gt;

F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR4&gt;

F:436-452/Domain: transmembrane #status predicted <TM>

F:453-477/Domain: cytosolic #status predicted &lt;CYT&gt;

F:32-38,36-45,152-176,154-194,218-266,302-345/disulfide bonds: #status experimental

F:67,95,121,178,205,241,254,280,325,338,350,412/Binding site: carbohydrate (Aan) (covalent)

Query Match 57.0%; Score 2520; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 2.1e-113;

Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSWIRHGPAMARLWGFVWFWRAAFACPTSCSCASRIWCSDPSPGIYAFPLRP 60  
DB 1 MSSWIRHGPAMARLWGFVWFWRAAFACPTSCSCASRIWCSDPSPGIYAFPLRP 60  
QY 61 NSVDPENITFIYANOKRELIINDDVAYVGLRNLTIVDSGLKFVAHKAFLKNSNQHI 120  
DB 61 NSVDPENITFIYANOKRELIINDDVAYVGLRNLTIVDSGLKFVAHKAFLKNSNQHI 120  
QY 121 NFRNKLTSLSRKHFRHLDSELIIVGNPFTCSCDIMWIKTLQBAKSSPTDOLYCLNES 180  
DB 121 NFRNKLTSLSRKHFRHLDSELIIVGNPFTCSCDIMWIKTLQBAKSSPTDOLYCLNES 180  
QY 181 SKNIPLANLOIPNCGLPANLAANLTVEEGKSTITLSCVAGDPVPMYVDGNLVSKM 240  
DB 181 SKNIPLANLOIPNCGLPANLAANLTVEEGKSTITLSCVAGDPVPMYVDGNLVSKM 240

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Db      181 SKNIPPLANLOIPNCGLPBANLAAPNLTVBEGKSTITLSCSYAGDPVPMYTDVGNLYKMK 240
Qy      241 NETSHTQGSIRITNISDDSGKOISCAVENLVGEDQDSVNLTVHFAPTITFLESPTSDDH 300
Db      241 NETSHTQGSIRITNISDDSGKOISCAVENLVGEDQDSVNLTVHFAPTITFLESPTSDDH 300
Qy      301 WCIPFTVGNPKPALOMFYNGALINESKYICTKIHTVNTHEHGCLQLDNPTMNNGDYT 360
Db      301 WCIPFTVGNPKPALOMFYNGALINESKYICTKIHTVNTHEHGCLQLDNPTMNNGDYT 360
Qy      361 LIANKYGEDEKOISAHFMGMPGIDGAPNPYDVEYEDGTANDIGDTNRSNEIPST 420
Db      361 LIANKYGEDEKOISAHFMGMPGIDGAPNPYDVEYEDGTANDIGDTNRSNEIPST 420
Qy      421 DVTDKTRGRLHSYAAVVAVIASVVGFCLLVNLFLKLARSHKFGMKG 466
Db      421 DVTDKTRGRLHSYAAVVAVIASVVGFCLLVNLFLKLARSHKFGMKG 466

```

## RESULT 6

```

A35104
brain-derived neurotrophic factor receptor precursor, short splice form - mouse
N:Alternate names: truncated receptor tyrosine kinase trkB
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 11-Jun-1999
C:Accession: A35104
R:Klein, R.; Conway, D.; Parada, L.F.; Barbacid, M.
Cell 61, 647-656, 1990
A:Title: The trkB tyrosine protein kinase gene codes for a second neurogenic receptor th
A:Reference number: A35104; MUID:90263089; PMID:2160854
A:Accession: A35104
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-476 <KLE>
A:Cross-references: GB:W33985; NID:g202158; PIDN:AAA40482.1; PID:g202159
C:Comment: This form of the receptor is missing the protein kinase domain.
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C:Keywords: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; t
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-476/Product: brain-derived neurotrophic factor receptor, short splice form #status
F:32-434/Domain: extracellular #status predicted <EXT>
F:92-915/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:116-1138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:435-451/Domain: cytosolic #status predicted <CYT>
F:452-476/Domain: transmembrane #status predicted <TM>
F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aen) (cova

```

```

Query Match      51.8%; Score 2292.5; DB 1; Length 476;
Best Local Similarity 89.7%; Pred. No. 1.5e-102; Indels 1; Gaps 1;
Matches 418; Conservative 27; Mismatches 20;
Qy      1 MSWIRHMGPMARLWGFVWFMRAAFACPTSCCKSASRIWCSDPSPGIVAFPLRP 60
Db      1 MSPPLKMHGPMALWGLCLVLGFWASLACPTSCCKSASRIWCSDPSPGIVAFPLRP 60
Qy      61 NSVDPENITEIFIANQRLIINEDVEAYVGLRNLTIVDSGLKFVAHKAFLKNSNTQHI 120
Db      61 NSVDPENITEIFIANQRLIINEDVEAYVGLRNLTIVDSGLKFVAHKAFLKNSNRHI 120
Qy      121 NPTNKTLSLSRKAFRHLIDSEILVGNPFTCSCDIMWIKTLQAKSSPDYODLYCINES 180
Db      121 NPTNKTLSLSRRFRHLIDSDLLTGPFPCSCDIIWMLKTLQETKSPDYODLYCINES 180
Qy      181 SKNIPPLANLOIPNCGLPBANLAAPNLTVBEGKSTITLSCSYAGDPVPMYTDVGNLYKMK 240
Db      181 SKNIPPLANLOIPNCGLPBANLAAPNLTVBEGKSTITLSCSYAGDPVPMYTDVGNLYKMK 240
Qy      241 NETSHTQGSIRITNISDDSGKOISCAVENLVGEDQDSVNLTVHFAPTITFLESPTSDDH 300
Db      241 NETSHTQGSIRITNISDDSGKOISCAVENLVGEDQDSVNLTVHFAPTITFLESPTSDDH 300

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Qy      301 WCIPFTVGNPKPALOMFYNGALINESKYICTKIHTVNTHEHGCLQLDNPTMNNGDYT 360
Db      301 WCIPFTVGNPKPALOMFYNGALINESKYICTKIHTVNTHEHGCLQLDNPTMNNGDYT 360
Qy      361 LIANKYGEDEKOISAHFMGMPGIDGAPNPYDVEYEDGTANDIGDTNRSNEIPST 420
Db      361 LIANKYGEDEKOISAHFMGMPGIDGAPNPYDVEYEDGTANDIGDTNRSNEIPST 420
Qy      421 DVTDKTRGRLHSYAAVVAVIASVVGFCLLVNLFLKLARSHKFGMKG 466
Db      421 DVTDKTRGRLHSYAAVVAVIASVVGFCLLVNLFLKLARSHKFGMKG 466

```

## RESULT 7

```

A55178
neurotrophin receptor trkC precursor - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
C:Accession: A55178
R:McGregor, L.M.; Baylín, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
Genomics 22, 267-272, 1994
A:Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignme
A:Reference number: A55178; MUID:95104834; PMID:7806211
A:Accession: A55178
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-825 <MG>
A:Cross-references: GB:U05012; NID:g442389; PIDN:AAA75374.1; PID:g442390
C:Gene: GDB:NTRK3
A:Map position: 15q24-15q25
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C:Keywords: alternative splicing; ATP; growth factor receptor
F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F:516-817/Domain: protein kinase homology <KIN>
F:544-552/Region: protein kinase ATP-binding motif

```

```

Query Match      51.8%; Score 2289; DB 2; Length 825;
Best Local Similarity 54.4%; Pred. No. 4e-102;
Matches 466; Conservative 111; Mismatches 199; Indels 80; Gaps 17;
Qy      10 PAAARLW----GFCWL-VGFMRAAFACPTSCCKSASRIWCSDPSPGIVAFPLRP--- 60
Db      7 PACCFMRIRPLDSVWLDVVG---SVLACPANCVCSTETNCRPPDGNL-FPLLEGQDS 62
Qy      61 -----NSVD-PENITEIFIANQRLIINEDVEAYVGLRNLTIVDSGLKFVAHKA 110
Db      63 GNSNGASINITYTISRNTSIHLENWRSLLTNAVDMLTYGLOKLTIKNSGLRSIOPRA 122
Qy      111 FLKNSNLOHINPTNKTLSLSRKAFRHLIDSEILVGNPFTCSCDIMWIKTLQOE-AKSSP 169
Db      123 FAKNPHRIRYNLSNRITLTSWQLFQTLRLQLQEQNFNCGCDIIMWLMQEGSAKL 182
Qy      170 DTQDLYCLNESSKNIPLANLOIPNCGLPBANLAAPNLTVBEGKSTITLSCSYAGDPVPMY 229
Db      183 NSQNLVCINADGSQLPLFRNNISQCDLPEISVSHVNLTVBEGNAVITTCGSGSPPLDVD 242
Qy      230 WDVGNLYS-----KNNETSHTQGSIRITNISDDSGKOISCAVENLVGEDQDSVNLTVH 284
Db      243 WITVGLQISNTHQNTLWVAHINLTVAVTSDNGFTLTJLAENNVGASNSVALITVY 302
Qy      285 FAPTITLESPTSDDHWCIPFTVGNPKPALOMFYNGALINESKYICTKIHTVNTHEHGCLQ 343
Db      303 YPRVYVSLSEPRRLRHCIFVVRGNRPPLTHLHNGQPLRESKII-----HVEYIQ 354
Qy      344 -----GCLQLDNPTMNNGDYTLLANKYGEDEKOISAHFMGMPGIDGAPNPYD- 394
Db      355 EGEISBQCLLFNRPTHYNNGNVYLLANPLGTANQTINGHFLXEP-----FPSTSD 405

```

QY 395 --VIEDYGTAAANDIGDTTRNSNEIPSTDTYDKTGRHLSVYAVVYASVGC-LLVNL 451  
Db 406 NLFLEDEV-----SPTPTTYTHKREBDFGVSAVGLAARA--CVLLVL 449  
QY 452 FLI--KLARHSKFGMKGPASVISNDSDASPLHHISNGSNTSPSSBEGGPPAVIIGMTKIP 509  
Db 450 FVMINKYGRSKFGMKGPVAVISGEEDSAPLHHINNGITTPSSLDAGPDTVIYGMTRIP 509  
QY 510 VIENPOYFGITNSQLKPDFTYQHIKRNIVYKRELGGAGKGVFLACYNLCPEODKILV 569  
Db 510 VIEHPQYFROGHCHCKEDDYQHIKRDIVLKRELGGAGKGVFLACYNLSPTKDMKLV 569  
QY 570 AVKTLQASDNARKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMVFEYMKGGDLNKL 629  
Db 570 AVKALQDPTLAARKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMVFEYMKGGDLNKL 629  
QY 630 RAHGPDAVLASGNP---PTELQSQMLHIAQOIAAGVTVLASQHFVHRDLATRNCLVGE 686  
Db 630 RAHGPDAVLASGNP---PTELQSQMLHIAQOIAAGVTVLASQHFVHRDLATRNCLVGE 689  
QY 687 NLVYKIDFGMSRDVYSTDYRVCGHTMLPIRMPPESIMYRKTTESDYMSLGVLMET 746  
Db 690 NLVYKIDFGMSRDVYSTDYRVCGHTMLPIRMPPESIMYRKTTESDYMSLGVLMET 749  
QY 747 FTYGKOPMYOLSNNEVEICTQGRVLTQRPRTCPQEVYELMGCMQREPHMKXIKGITHL 806  
Db 750 FTYGKOPMYOLSNNEVEICTQGRVLTQRPRTCPQEVYELMGCMQREPHMKXIKGITHL 809  
QY 807 LQNLAKASPVYLDILG 822  
Db 810 LHALGKATPIYLDILG 825

## RESULT 8

173632  
neurotrophin-3 receptor precursor - human  
N:Alternate names: receptor tyrosine kinase trkC  
N:Contain: protein-tyrosine kinase (EC 2.7.1.112)  
C:Species: Homo sapiens (man)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I73632  
J:Shelton, D.L.; Sutherland, J.; Grifp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.  
R:Neurosci. 15, 477-491, 1995  
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extracell  
A:Reference number: 156557; MUID:95123473; PMID:7823156  
A:Accession: I73632  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-839 <RES>  
A:Cross-references: UNIPROT:Q16288; GB:S76475; NID:g913721; PIND:AA03111.1; PID:g913722  
C:Genetic: A:Gene: GDB:NTRK3, TRKC  
A:Cross-references: GDB:127899; OMIM:191316  
A:Map position: 15q24-15q25  
C:Function: A:Description: regulation of nervous system development; receptor for neurotrophin-3  
C:Superfamily: nerve growth factor receptor; high affinity; leucine-rich alpha-2-glycop  
C:Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phos  
P:1.31/Domin: signal sequence #status predicted <SIG>  
F:33-839/Product: neurotrophin-3 receptor #status predicted <MAT>  
F:33-436/Domin: extracellular #status predicted <EXT>  
F:79-103/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:104-127/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:128-150/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:151-162/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:437-453/Domin: transmembrane #status predicted <TM>  
F:454-839/Domin: cytosolic #status predicted <CYT>  
F:536-831/Domin: protein kinase homology <KIN>  
F:544-552/Region: protein kinase ATP-binding motif  
F:72,79,133,153,203,218,232,252,267,294,375,386/Binding site: carbohydrate (Asn) (cc  
F:572/Active site: lys #status predicted  
F:709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
F:834/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 51.5%; Score 2277; DB 1; Length 839;  
Best Local Similarity 53.7%; Pred. No. 1,5e-101;  
Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;

QY 10 PAMARLW-----GFCWL-VVGFRAAPACPTSCSKCSARICWSDPSGVAPRLRR--- 60  
Db 7 PAKCSFMRITFLASWLDIVG---SVLACPAVCCKTETINCRPDDGNL-FPLBSQDS 62  
QY 61 -----NSVD-PENITEIFIANOKRLEI INEDVBAVVGRLNITVDSGLKFAHKA 110  
Db 63 GNSGNANINITD ISNRTSIHLENMRSRLTLAAVMELYTGKLTIKSGSLRISQRA 122  
QY 111 FLKNSUQIINFRANKLTSLSRKFRHLDELIVGNPPTGCDIMITLDE-AKSGP 169  
Db 123 FAKNPRLRYINLSNRLTTLISWQLFDTLSRELQLQNFENCSCDIRMDLWEOGKAKL 182  
QY 170 DTODLYCLNESSKNIPLANQIPNCGPSANLAPMLTYEBSGSLTSGSVADPVPNNY 229  
Db 183 NSQNLICINADSGQLPFRKNISQCDLPBISVSHVNLTYREGDNNAVITTCGSGSLPDPVD 242  
QY 230 MDVGNLVS-----KHNETSHTQSLRTNITSSDSGKOISCYAENLVGEDSDVNLTV 284  
Db 243 MIVTGLQSIINTQTNLMTVHAINTLVVNTSENGFTLTCLAEVNVGMSNLSVALTV 302  
QY 285 FAPTITFLESPTSDHMCIPFTYKGNPKPALQFPYNGAILNBSKTYICTKHVNTTEYH- 343  
Db 303 YPRVAVSLBEPELRLEBHCIEFVVRGNPPTLHNLHNGQPRBSKII-----HVEYQ 354  
QY 344 -----GCLQDNPETHANNNGDYTLIAKNEYGKQEKQISAFPMQPGIDGANDPNYPD--- 394  
Db 355 EGEISRGCLLFNKPETHYNNQNTYLLAKNPLGTANQITNGHFLKP-----FPESTD 405  
QY 395 --VIEDYGTAAANDIGDTTRNSNEIPSTDTYDKTGRHLSVYAVVYASVGC-LLVNL 451  
Db 406 NLFLEDEV-----SPTPTTYTHKREBDFGVSAVGLAARA--CVLLVL 449  
QY 452 FLI--KLARHSKFGMKGPASVISNDSDASPLHHISNGSNTSPSSBEGGPPAVIIGMTKIP 509  
Db 450 FVMINKYGRSKFGMKGPVAVISGEEDSAPLHHINNGITTPSSLDAGPDTVIYGMTRIP 509  
QY 510 VIENPOYFGITNSQLKPDFTYQHIKRNIVYKRELGGAGKGVFLACYNLCPEODKILV 569  
Db 510 VIEHPQYFROGHCHCKEDDYQHIKRDIVLKRELGGAGKGVFLACYNLSPTKDMKLV 569  
QY 570 AVKTLQASDNARKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMVFEYMKGGDLNKL 629  
Db 570 AVKALQDPTLAARKDFRBAELTNLQHEHIVKRYGVCGVGDPLIMVFEYMKGGDLNKL 629  
QY 630 RAHGPDAVLASGNP---PTELQSQMLHIAQOIAAGVTVLASQHFVHRDLATRNCLVGE 686  
Db 630 RAHGPDAVLASGNP---PTELQSQMLHIAQOIAAGVTVLASQHFVHRDLATRNCLVGE 689  
QY 687 NLVYKIDFGMSRDVYSTDYRVCGHTMLPIRMPPESIMYRKTTESDYMSLGVLMET 746  
Db 690 NLVYKIDFGMSRDVYSTDYRVCGHTMLPIRMPPESIMYRKTTESDYMSLGVLMET 749  
QY 747 FTYGKOPMYOLSNNEVEICTQGRVLTQRPRTCPQEVYELMGCMQREPHMKXIKGITHL 806  
Db 750 FTYGKOPMYOLSNNEVEICTQGRVLTQRPRTCPQEVYELMGCMQREPHMKXIKGITHL 809  
QY 807 LQNLAKASPVYLDILG 822  
Db 810 EPOGRINIKIYVILHALGKATPIYLDILG 839  
RESULT 9  
C39667  
brain-derived neurotrophic factor receptor precursor, splice form T2 - rat  
N:Alternate names: truncated receptor tyrosine kinase trkB.T2  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 09-Jul-2004  
C:Accession: C39667

R;Middlemas, D.S.; Lindberg, R.A.; Hunter, T.  
 Mol. Cell. Biol. 11, 143-153, 1991  
 A>Title: trkb, a neural receptor protein-tyrosine kinase: evidence for a full-length and  
 A/Reference number: A39667; MUID:91094826; PMID:1846020  
 A/Accession: C39667  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-474 <MID>  
 A/Cross-references: UNIPROT:Q63604; GB:M55293; NID:9207477; PID:AAA42281.1; PID:9207478  
 C/Comment: This form of the receptor is missing the protein kinase domain.  
 C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr  
 C/Keywords: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; t  
 F/1-31/Domain: signal sequence #status predicted <SIG>  
 F/32-474/Product: brain-derived neurotrophic factor receptor, splice form T2 #status pre  
 F/32-434/Domain: extracellular #status predicted <EXT>  
 F/67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F/116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F/139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #atypical <LR  
 F/435-451/Domain: transmembrane #status predicted <TM>  
 F/452-474/Domain: cytosolic #status predicted <CYT>  
 F/67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aan) (coval

Query Match 51.5%; Score 2275.5; DB 1; Length 474;  
 Best local similarity 89.1%; Pred. No. 9.5e-102;  
 Matches 415; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MSSIRRHGPMALNGFCMLVGFWRAPACPTSCSKSARITCSDPSPTGIVAPRLRP 60  
 Db 1 MSPWRHGMAMLMGCLLVGFWRASLACPMSCSTTRITWCTEPPGIVAPRLRP 60  
 Qy 61 NSVDPENITFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKNSNLOHI 120  
 Db 61 NSIDPENITELLINOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKNSNLRHI 120  
 Qy 121 NFRNKLTSLSRKHFRLDSEILVGNPFTSCDINWIKTLQBAKSSPTODLYCLNES 180  
 Db 121 NFRNKLTSLSRRHFRHLDSDILITGNPFTSCDINWIKTLQETKSSPTODLYCLNES 180  
 Qy 181 SKNIPLANLOIPNCGLPBANLAAPNLTVBEKGSITLSCSVAGDPVPMYVGNLVSKM 240  
 Db 181 SKNIPLANLOIPNCGLPBANLAAPNLTVBEKGSITLSCSVAGDPLPTLYVGNLVSKM 240  
 Qy 241 NETSHTOGSLRITNISDDSGKOISCAENLVGEDQSVNLTVFAPPTITLESPTSDH 300  
 Db 241 NETSHTOGSLRITNISDDSGKOISCAENLVGEDQSVNLTVFAPPTITLESPTSDH 300  
 Qy 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVTHNTEHYGCLQDNPTHANNQDYT 360  
 Db 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVTHNTEHYGCLQDNPTHANNQDYT 360  
 Qy 361 LIANREYKDEKQISAFPMGPGIDGAPNPNVYEDYGTANDIGDTTNRSENPST 420  
 Db 361 LMANREYKDEKQISAFPMGPGIDGAPNPNVYEDYGTANDIGDTTNRSENPST 419  
 Qy 421 DVYDKTGRHLSYAVVAVVIVASVGFCLLVMLFLTKLARHSKFGMKG 466  
 Db 420 DVADQTNREHLSYAVVAVVIVASVGFCLLVMLFLTKLARHSKFGMKG 465

RESULT 10  
 B39667  
 brain-derived neurotrophic factor receptor precursor, splice form T1 - rat  
 N/Alternate names: truncated receptor tyrosine kinase trkb-T1  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 09-Jul-2004  
 C/Accession: B39667  
 R;Middlemas, D.S.; Lindberg, R.A.; Hunter, T.  
 Mol. Cell. Biol. 11, 143-153, 1991  
 A>Title: trkb, a neural receptor protein-tyrosine kinase: evidence for a full-length and  
 A/Reference number: A39667; MUID:91094826; PMID:1846020  
 A/Accession: B39667  
 A/Status: preliminary

A/Molecule type: mRNA  
 A/Residues: 1-476 <MID>  
 A/Cross-references: UNIPROT:Q63604; GB:M55292; NID:9207475; PID:AAA42280.1; PID:9207476  
 C/Comment: This form of the receptor is missing the protein kinase domain.  
 C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr  
 C/Keywords: alternative splicing; glycoprotein; growth factor receptor; tandem repeat; t  
 F/1-31/Domain: signal sequence #status predicted <SIG>  
 F/32-476/Product: brain-derived neurotrophic factor receptor, splice form T1 #status pre  
 F/32-434/Domain: extracellular #status predicted <EXT>  
 F/67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F/116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F/139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #atypical <LR  
 F/435-451/Domain: transmembrane #status predicted <TM>  
 F/452-476/Domain: cytosolic #status predicted <CYT>  
 F/67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Aan) (coval

Query Match 51.5%; Score 2275.5; DB 1; Length 476;  
 Best local similarity 89.1%; Pred. No. 9.5e-102;  
 Matches 415; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MSSIRRHGPMALNGFCMLVGFWRAPACPTSCSKSARITCSDPSPTGIVAPRLRP 60  
 Db 1 MSPWRHGMAMLMGCLLVGFWRASLACPMSCSTTRITWCTEPPGIVAPRLRP 60  
 Qy 61 NSVDPENITFIANOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKNSNLOHI 120  
 Db 61 NSIDPENITELLINOKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKAFKNSNLRHI 120  
 Qy 121 NFRNKLTSLSRKHFRLDSEILVGNPFTSCDINWIKTLQBAKSSPTODLYCLNES 180  
 Db 121 NFRNKLTSLSRRHFRHLDSDILITGNPFTSCDINWIKTLQETKSSPTODLYCLNES 180  
 Qy 181 SKNIPLANLOIPNCGLPBANLAAPNLTVBEKGSITLSCSVAGDPVPMYVGNLVSKM 240  
 Db 181 SKNIPLANLOIPNCGLPBANLAAPNLTVBEKGSITLSCSVAGDPLPTLYVGNLVSKM 240  
 Qy 241 NETSHTOGSLRITNISDDSGKOISCAENLVGEDQSVNLTVFAPPTITLESPTSDH 300  
 Db 241 NETSHTOGSLRITNISDDSGKOISCAENLVGEDQSVNLTVFAPPTITLESPTSDH 300  
 Qy 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVTHNTEHYGCLQDNPTHANNQDYT 360  
 Db 301 WCIPFTYKGNPKPALQWFGYNGAILNESKYICTKIHVTHNTEHYGCLQDNPTHANNQDYT 360  
 Qy 361 LIANREYKDEKQISAFPMGPGIDGAPNPNVYEDYGTANDIGDTTNRSENPST 420  
 Db 361 LMANREYKDEKQISAFPMGPGIDGAPNPNVYEDYGTANDIGDTTNRSENPST 419  
 Qy 421 DVYDKTGRHLSYAVVAVVIVASVGFCLLVMLFLTKLARHSKFGMKG 466  
 Db 420 DVADQTNREHLSYAVVAVVIVASVGFCLLVMLFLTKLARHSKFGMKG 465

RESULT 11  
 I51259  
 tyrosine kinase C receptor - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 09-Jul-2004  
 C/Accession: I51259  
 R;Garner, A.S.; Large, T.H.  
 Neuron 13, 457-472, 1994  
 A>Title: Isoforms of the avian TrkC receptor: a novel kinase insertion dissociates trans  
 A/Reference number: I51259; MUID:94338700; PMID:8060621  
 A/Accession: I51259  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-852 <GAR>  
 A/Cross-references: UNIPROT:Q91044; GB:S74248; NID:g712820; PID:AA031699.1; PID:g712821  
 C/Genetics: trkb  
 C/Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr  
 F/79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>



F:538-844/Domain: protein kinase homology <KIN>

Query Match	51.0%	Score 2252.5	DB 2	Length 852
Best Local Similarity	52.7%	Pred. No. 2.3e-100		
Matches 463	Conservative 114	Mismatched 204	Indels 97	Gaps 18
QY	10	PAMARLWQ--FCWLIVG--FWRAAFACPTSCSKCSASRIMCSDSPSPTVAAPRLEP-----	60	
Db	7	PTKCFMFAVPLIMSWIDYILSLVLAACPNALCCKSKIDINCKRPDDGNL--PRLLEGDSGS	65	
QY	61	-----NSVD--PENITEIFIANOKRLIINEDDAVYGLRNLTIVDSGLKFAHKAFLK	113	
Db	66	NGNTSINITDISRNITSIHIEBWKMIQLTNAVDMELTYGLQLTIRNSGLRNIQRAFAK	125	
QY	114	NSNLQHNFTNRKLTLSLRKRRHLDSELLIVGNPFTSCSDIMYTKLQF--AKSSPTQ	172	
Db	126	NPHLEFIDLSGRRLTTLTSQWLFQTLRLPDLRLERNPFNCSQIRIKIOLWQERGANLSQ	185	
QY	173	DLVCNESSKNPLANLOIPNCGPLSANLAAPNLTVBEKSTLTSCSVAGDVPFMYMDV	232	
Db	186	QLHCNLTAVLLNNMTIQCDLBEISVSHNLTVBEGENAVITCNSGSSLPDVMTV	245	
QY	233	GNLVS-----KAMNETSHQSGLRITNISDDSGKOISCAVENLYGEODSVNLTVHPAP	287	
Db	246	ADLHSINTHTLMTNTVNAIILTLVNVTSBDNGELFTCAENNVGMSNASTLITVYPP	305	
QY	288	TITPLESTPSDHHMCIPTFYKGNPKPALOWFNQALIMESKTICTKIHVNTTEH----	343	
Db	306	RILTEEPVHLHCHIAFAVHNPAPTLMLNLGVLRETEIIL-----HMEFYQGE	357	
QY	344	---GGLQDNPTHMNGDYTLTAKKEYGDKQISAHFPMGWGIDGANPNPD-----V	395	
Db	358	VSEGLLRNKPRTYHNGVITVATQDLSANOTIKGHFLERK-----PPESTDNFV	408	
QY	396	IYEDYGTAAINDIGDTTNRSEIIPSTDVTDKTRERHLYVAVVVIVASVVGFC--LLVMEFL	454	
Db	409	STGDY-----EVSPT-----PRITVTHKPREDFGVSIAVGLAFA--CVLVLVLFIM	454	
QY	455	--KLARHKFKMGKAGSAVSIINDDDASPLHNISSNGSNTPSSSEGGPDVITIGTKIPYTE	512	
Db	455	INKYRRRSFKMGKGPAAVIVSGEDASPLHNIHGILTPPSSLDAGDPTVIGMTIRIPLYE	514	
QY	513	NPOYEGITNSOLKPTFVOHIRKRNIVLKRLEGEAGFVFLAACNCLCPEDOKILVAVK	572	
Db	515	NPOYRQGNCHCKPTTYOHLKRBDIVLKRLEGEAGFVFLAACNCLSPYDNRMLVAVK	574	
QY	573	TLKQASDNARKDFHREABILLTNLOHSHIVKPYGVCSVGGDPLIMVEYMGSGDINFLRAH	632	
Db	575	ALKQDPTLARKDFQREABELLTNLOHSHIVKPYGVGGDGPPLIMVEYMGSGDINFLRAH	634	
QY	633	GPDVLAABGNP---PTBELTOSQMLHIAQOILAGMYTLLASQHFVRHDLATRNCLVGENILL	689	
Db	635	GPDAMILVDGQPRQAKGELGLSOMLHIASQIASGMVYLLASQHFVRHDLATRNCLVGANILL	694	
QY	690	VKIGFGMSRDVYSTDYR-----VGGHMILLIRMMPPES	724	
Db	695	VKIGFGMSRDVYSTDYRBEGRPKQULSTAMORHRLAPPAAYVGGHMLIRMMPPES	754	
QY	725	IMYRKFTTESDVMSLGVVLMELFTYQKQWYOLSSNNEVEICTOGKVLQRPPTCQEVYE	784	
Db	725	IMYRKFTTESDVMSLGVVLMELFTYQKQWYOLSSNNEVEICTOGKVLQRPPTCQEVYD	814	
QY	785	IMLGCWOREPHNRKNIKGIHTLLQNLAKASPVYLDILG	822	
Db	815	IMLGCWOREPHNRKNIKGIHTLLQNLAKASPVYLDILG	852	

C:\Date: 17-Jan-1992 #sequence 17-Jan-1992 #text\_change 09-Jul-2004

R1Lamballe, F.; Klein, R.: Barbacid, M.  
Cell 66, 967-979, 1991  
A1Title: trkC, a new member of the trk family of tyrosine protein kinases, is a receptor  
A1Reference number: A40026; MUID:91364178; PMID:1653651  
A1Accession: A40026  
A1Molecule type: mRNA  
A1Residues: 1-825 <LAM>  
A1Cross-references: UNIPROT:P24786; GB:M80800; NID:G164638; PID:AAA31130.1; PID:G164639  
A1Experimental source: adult brain  
C1Function:  
A1Description: regulation of nervous system development; receptor for neurotrophin-3  
C1Superfamily: nerve growth factor receptor; high affinity; leucine-rich alpha-2-glycoprotein  
C1Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phospho  
F1.1-31/Domain: signal sequence #status predicted <SIG>  
F1.32-825/Product: neurotrophin-3 receptor #status predicted <MAT>  
F1.32-436/Domain: extracellular #status predicted <EXT>  
F1.79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
F1.104-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F1.128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
F1.151-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR4>  
F1.437-485/Domain: transmembrane #status predicted <TM>  
F1.454-825/Domain: cytosolic #status predicted <CYT>  
F1.536-811/Domain: protein kinase homology <KIN>  
F1.544-552/Region: protein kinase ATP-binding motif  
F1.68, 72, 79, 133, 163, 203, 218, 233, 259, 267, 272, 294, 338/Binding site: carboxydrate (Asn)  
F1.572/Active site: lys #status predicted  
F1.709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
F1.820/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match	49.3%;	Score 2178;	DB 1;	Length 825;
Best Local Similarity	52.9%;	Pred. No. 7.8e-97;		
Matches 454;	Conservative 105;	Mismatches 214;	Indels 86;	Gaps 19

RESULT 12  
A40026  
neurotrophin-3 receptor precursor - pig  
N:Alternate names: receptor tyrosine kinase trkC  
M:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C:Species: Sus scrofa domestica (domestic pig)



Db 507 RPIVENPQYRQCHNCKPPTVOHTRKRDIVLKRLEBGAFGKVLAECTNLSPIYVK 566  
 QY 567 ILVAVKTLKDSADNARKDFHREAEITLNLQEHYLYKFGVCEGDPPLIMEYMKGDIN 626  
 Db 567 MLVAVKOLKDPFLAARQDFQREAEITLNLQEHYLYKFGVCGDDPPLIMVEYMKHGLN 626  
 QY 627 KFLRAHGPDAVLMAEGND--PTEITQSOMLHIAQOIAAGNVYLASQHFVARDLATRNCL 683  
 Db 627 KFLRAHGPDAVLMAEGND--PTEITQSOMLHIAQOIAAGNVYLASQHFVARDLATRNCL 686  
 QY 684 VGEMLLVKIGDPMGRSDVYSDYRVGHTMLPIRMPPEISIMYRKFTTESDWSLSGLVL 743  
 Db 687 VGANLVVIGDPMGRSDVYSDYRVGHTMLPIRMPPEISIMYRKFTTESDWSLSGLVL 746  
 QY 744 WEITFYGKQPMYQLSNNVEICTQGRYLQRPCTQPEVEYELMGCMQREPMRNKIKGI 803  
 Db 747 WEITFYGKQPMYQLSNNVEICTQGRYLQRPCTQPEVEYELMGCMQREPMRNKIKGI 806  
 QY 804 HTLLQNLAKASPVYLDILG 822  
 Db 807 YKILHALGKATPIYLDILG 825

## RESULT 13

S35695  
 neurotrophin-3 receptor precursor - chicken  
 N:Alternate names: receptor tyrosine kinase trkc  
 N:Contains: protein-tyrosine kinase (BC 2.7.1.112)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 10-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S35695  
 R:Okazawa, H.; Kamei, M.; Kanazawa, I.  
 FEBS Lett. 329, 171-177, 1993  
 A:Title: Molecular cloning and expression of a novel truncated form of chicken trkc.  
 A:Reference number: S35695; MUID:93359043; PMID:8394830  
 A:Accession: S35695  
 A:Molecule type: mRNA  
 A:Residues: 1-803 <OK>  
 A:Cross-references: UNIPROT:Q91044; EMBL:X59669; NID:9416429; PIDN:CAA42202.1; PID:94164  
 A>Note: the authors translated the codon AAC for residue 105 as Val, CIG for residue 108  
 C:Function: regulation of nervous system development; receptor for neurotrophin-3  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr  
 C:Keywords: alternative splicing; ATP; autophosphorylation; brain; glycoprotein; growth  
 protein kinase  
 F:1-10/Domain: signal sequence #status predicted <SIG>  
 F:11-803/Product: neurotrophin-3 receptor #status predicted <MAT>  
 F:11-417/Domain: extracellular #status predicted <EXT>  
 F:58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:130-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR  
 F:418-434/Domain: transmembrane #status predicted <TM>  
 F:435-803/Domain: cytosolic #status predicted <CT>  
 F:514-795/Domain: protein kinase homology <KIN>  
 F:522-530/Region: protein kinase ATP-binding motif  
 F:47-51,58,142,182,197,211,238,246,251,273,354,367/Binding site: carbohydrate (Aam) (cov  
 F:550/Active site: lys #status predicted  
 F:687/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte  
 F:798/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 48.6%; Score 2149.5; DB 1; Length 803;  
 Best Local Similarity 53.3%; Pred. No. 1-7e-95;  
 Matches 448; Conservative 112; Mismatches 202; Indels 79; Gaps 18;  
 QY 19 CMLVGFWRAPACPTSCSKSASRIWCSDPSPGIAPRRLP-----NSVD-P 65  
 Db 5 CMRIASFADRLKLVLFKTD-----INCKPDDGML-FPLLEGQSGSSNGMTSINITDIS 56  
 QY 66 ENRIEIPFANQKLEIINEDVEAVGIRNTIYDSGLKFAHAKFLKNSMLQHNIFRN 125  
 Db 57 RNITSIHENKMNQTLNAVVMELTYGLRILIRNSGLRNIOPRAFGNPHLARYDLSGN 116

QY 126 KLTSLSKRHRRLDLSELILVGNPFTGSCDIMWIKTLQE-AKSSPDQDLYCLNBSSKNI 184  
 Db 117 RLTLTSQLQFQTLALFDLRLERNPFNCSDIRWIQLOKEKANIOSQQLHCMLDITAVI 176  
 QY 185 PLALQIPNCGLPBANLAAPLTYEBKSLITLSCSVAGDPVPMYMGVNLVS-----KH 239  
 Db 177 LLRRMNLTQCDLPEISVSHVNLTVREGENAVITNCGSPPLPDVMTADLHLSINTQTN 236  
 QY 240 MNETSHTQGSIRITNINISDDSGKOISCAENLVGEDDQSVLVTHAPATITFLESPTS 299  
 Db 237 LMTNVAIINILTVNVSSENGFLITCIAENVGMSASVLLTYYPRIITLLEPVILH 296  
 QY 300 HWCIPFTVKNPKPALQMFNGAILNESKYICTKIHVTNTEYH-----GCLQDNPT 352  
 Db 297 EHCIAFVHGNPAFTLMLHNGQVLRTEII-----HMEFYQGSBEGCLLPNKPT 348  
 QY 353 HANNQDITLAKNEYGDEKQISAHFMGMFGIDGAAHPNPV-----VIYEDYGTANDI 407  
 Db 349 HYNNGNYTIVATNOLGSANQTIKGFLEKP-----PESTDNFVSIGDY-----EV 394  
 QY 408 GDTNRSNEIPSTDVDTKGRHEHLSYAVVYIASVGFCLLVNLFTLL--KLARHSKGM 464  
 Db 395 SPT-----PPIVTKRPEEDTGVSIANGLAFA--CULVLVFTMINKYGRSRKGM 445  
 QY 465 KGPASVLSNDSDASPLMHSNGSNTSPSSSEGPDAVIGMTKIPVIEPQYFGITNSQL 524  
 Db 446 KGPVAVISGEEDSAAT--HTST-TDTRFVYDAGDITVIGMTRLPVIEENPQYFGQHCH 502  
 QY 525 KPDTFVOHKKRNIVLKRLEGAGAFGVFLAECYNLCPEODKILVAVKTLKDSADNARKD 584  
 Db 503 KPDYVOHKKRDRVLKRLLEGAGAFGVFLAECYNLCPEODKILVAVKTLKDSADNARKD 562  
 QY 585 FHREAEITLNLQEHYLYKFGVCEGDPPLIMVEYMKHGDNKFRAHGPDAVLMAEGNP 644  
 Db 563 FHREAEITLNLQEHYLYKFGVCEGDPPLIMVEYMKHGDNKFRAHGPDAVLMAEGNP 622  
 QY 645 ---PTEITQSOMLHIAQOIAAGNVYLASQHFVARDLATRNCLVGENLVKIGDPMGRSDV 701  
 Db 623 RQAKGELGLSQMLHIAQOIASGMVYLASQHFVARDLATRNCLVGANLVVIGDPMGRSDV 682  
 QY 702 YSTDYRVGHTMLPIRMPPEISIMYRKFTTESDWSLSGLVLMEIFYQKPMYQLSNNE 761  
 Db 683 YSTDYRVGHTMLPIRMPPEISIMYRKFTTESDWSLSGLVLMEIFYQKPMYQLSNNE 742  
 QY 762 VIECTQGRYLQRPCTQPEVEYELMGCMQREPMRNKIKGIHTLLQNLAKASPVYLDIL 821  
 Db 743 VIECTQGRYLQRPCTQPEVEYELMGCMQREPMRNKIKGIHTLLQNLAKASPVYLDIL 802  
 QY 822 G 822  
 Db 803 G 803

## RESULT 14

TRRTB  
 nerve growth factor receptor precursor, high affinity - rat  
 N:Alternate names: receptor tyrosine kinase trka  
 N:Contains: protein-tyrosine kinase (BC 2.7.1.112)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: A41981  
 R:Meakin, S.O.; Suter, U.; Drinkwater, C.C.; Weicher, A.A.; Shooter, E.M.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2374-2378, 1992  
 A:Title: The rat trk proto-oncogene product exhibits properties characteristic of the s10  
 A:Reference number: A41981; MUID:92196121; PMID:11312719  
 A:Accession: A41981  
 A:Molecule type: mRNA  
 A:Residues: 1-799 <MEA>  
 A:Cross-references: UNIPROT:P35739; GB:M85214; NID:9207481; PIDN:AAA42286.1; PID:9207482  
 A>Note: sequence extracted from NCBI database (NCBI:88433, NCBI:88434)  
 A:Comment: in Genbank entry RATTTRKRC, residue 113.0, the source is designated as Rattus r  
 C:Function: The proto-oncogene trka is activated by gene fusion. The amino end of several

A:Description: regulation of nervous system development; receptor for nerve growth factor  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein  
 C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprotein  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>  
 F:33-424/Domain: extracellular #status predicted <EXT>  
 F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:425-441/Domain: transmembrane #status predicted <TMN>  
 F:442-799/Domain: cytosolic #status predicted <CYT>  
 F:511-791/Domain: protein kinase homology <KIN>  
 F:519-527/Region: protein kinase ATP-binding motif  
 F:67,121,130,204,255,264,320,325,331,361,404/Binding site: carbohydrate (asn) (covalent)  
 F:547/Active site: lys #status predicted  
 F:663/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
 F:794/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 43.0%; Score 1901; DB 1; Length 799;  
 Best Local Similarity 49.0%; Pred. No. 1.3e-83;  
 Matches 407; Conservative 112; Mismatches 254; Indels 58; Gaps 18;

QY 7 WHGPMARLWGFCLVYVGFMAAFAACPTSCSCAS-RWCSDBSPGIVAFPRLEP-NSV- 63  
 DB 12 WHRPA-----GLGLVYTSMLA-----CACASCRCTCCPVGSGIRCTRACTTLTLR 60  
 QY 64 ---DPNTEIFINOKRLIINEDVAYVGLNLITVDSGLKFAVHAKAFKSNIOHI 120  
 DB 61 GLRAGNLTLYVNGNDLQLEFEDQGLASLTIVSGLAFVAPDAHFPRLSHL 120  
 QY 121 NFRNKLTSLSRKPRHLDSLLILVGNPTGSCDINWIKTL-GEANSPPTQDLYCLNE 179  
 DB 121 NLSNNALESLSMKTVQGLSLQDLTLISGNPLHSCALIMLQWQEDLCGVYTOQLQSSGS 180  
 QY 180 SSKRIPLANLQIPRCGLPSANLAPNLVTEGSKITLSCVAPGPRVPMYDVGNLYSKH 239  
 DB 181 GDQFLPLQHNN--SCGVPSVVIQHPNNSVEVDVFLQCVGQALQADMLTELGGTA 238  
 QY 240 MNETSHTQGLRIT--NISDSGKOISCVENLVGEODSVNLTVHAPITFLASPTS 297  
 DB 239 TMKSGDLPSGLTLVNTSLANKKNTCAENVDGARVSVQVSF-PASVHLGAWE 297  
 QY 298 DHHWCIPFTVKNRPALQWPFYNGALINSEKYICTKI---HYNHTYHGLQJDNPTM 354  
 DB 298 QHHCIPFSDVQGPAPSLRPFNGSVLNETSFIFLOFLESALTMTMRHGLRLNQPLHV 357  
 QY 355 NNGVYTLIAKRYGKDEKOISAHFMGWDGIDGANPNYEDYGTAAIDGDTNRS 414  
 DB 358 NNGVYTLIAANPYQAAASIMAAFM-----DNPEFPEDEPIVPSFSPV-----DTNSTS 407  
 QY 415 NEISTDVTDTKGRBHSVAVVAVIA-SVGFCLLVMLFLKLARHSFGKMGPRASYISN 473  
 DB 408 R-----DPEVKDETPFGVSAVGLAVSAALFLSALLVLVKKCGORSFEGINRA-VLAP 461  
 QY 474 DDDASPLMHSNNTPPSSSEGGPDVAIVQMTKIPVLENPQYGTITNSQLKPTFYQHI 533  
 DB 462 EDGLAMSLHFWTLGGSSLSPTGKSGS-----QHIMENQYTS-----DTCVHI 508  
 QY 534 KKHNIYVLRKELGEGAFGVFLAECNLCPEBDKILVAVTKLKAASDNARKQFHRBAELT 593  
 DB 509 KRQDIILLMELGEGAFGVFLAECNLLNDQKMLVAKALKETSENARQDFHREBAELT 568  
 QY 594 NLOHHTYKFGVCEGDPILMVPEYMGDPLNFKLHAGSDAIVLMEGN--PPELTQS 651  
 DB 569 MLOHHTYKFGVCEGDPILMVPEYMGDPLNFKLHAGSDAIVLMEGN--PPELTQS 628  
 QY 652 QMLHIAQOIAAGMYVLASQHFVHDLATRNCLVGENILVKIGDQMSRDYVSTDYRVG 711  
 DB 629 QLLAVASVAAAGMYVLASLHFVHDLATRNCLVQGLVAVKIGDQMSRDYVSTDYRVG 688  
 QY 712 HTMLPIRMPPESIMYRKFTTESDVWSLGVVLMELFTYGKOPWQLSNNEVIECTIGGRV 771

DB 689 RMLPPIRMPPESILTRKSTESDVWSFGVVLMEIFTYGQPYQLSNNTAIECTIGGR 748  
 QY 772 LQRPRTQPEVYELMLGQWREBPMRNKINGITLQLNLAASPVYLDIG 822  
 DB 749 LERPRACPPPVYALMGQWREBQQRISMVDVARIQALAAQAPPSYLDVIG 799

# RESULT 15

TVRHTT  
 Nerve growth factor receptor precursor, high affinity - human

N:Alternate names: receptor tyrosine kinase trkA  
 N:Contents: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1988 #sequence, revision 30-Jun-1991 #text, change 11-Jun-1999  
 C:Accession: A30124; S02366; A25184

R:Martin-Zanca, D.; Osham, R.; Mitra, G.; Copeland, T.; Barbacid, M.  
 Mol. Cell. Biol. 9, 24-33, 1989

A:Title: Molecular and biochemical characterization of the human trk proto-oncogene.  
 A:Reference number: A30124; MUID:89181575; PMID:2927393

A:Accession: A30124  
 A:Molecule type: mRNA

A:Residues: 1-790 <MAR1>  
 A:Cross-references: GB:M23102; NID:9339917; PIDN:AAA6770.1; PID:9339918

R:Kozma, S.C.; Redmond, S.M.S.; Xiao-Chang, F.; Saurer, S.M.; Groner, B.; Hynes, N.B.  
 EMBO J. 7, 147-154, 1988

A:Title: Activation of the receptor kinase domain of the trk oncogene by recombination w/  
 A:Reference number: S00261; MUID:88196074; PMID:2966065

A:Accession: S02366  
 A:Molecule type: mRNA

A:Residues: 393-758, 'HG', 761-790 <KOZ>  
 A:Cross-references: EMBL:X06704; GB:T00100; NID:937399; PIDN:CAA29888.1; PID:937400

R:Martin-Zanca, D.; Hughes, S.H.; Barbacid, M.  
 Nature 319, 743-748, 1986

A:Title: A human oncogene formed by the fusion of truncated tropomyosin and protein tyros  
 A:Reference number: A25184; MUID:86146854; PMID:2869410

A:Accession: A25184  
 A:Molecule type: mRNA

A:Residues: 393-762, 'SNATARMCTPGCKPMPRLHLSMTWMSMARQAGLGVSRNTGACQHP' <MAR2>  
 A:Cross-references: EMBL:X03541; NID:937402; PIDN:CAA27243.1; PID:937403

A:Note: the difference at the carboxyl end is due to a frameshift  
 C:Comment: The proto-oncogene trkA is activated by gene fusion. The amino end of several

C:Genetics:  
 A:Gene: GDB:NTRK1, TRK

A:Cross-references: GDB:127897; OMIM:191315  
 A:Map position: 1q21-1q22

C:Function:  
 A:Description: regulation of nervous system development; receptor for nerve growth factor

C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein  
 C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprotein

F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>

F:33-415/Domain: extracellular #status predicted <EXT>  
 F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F:416-432/Domain: transmembrane #status predicted <TMN>

F:433-790/Domain: cytosolic #status predicted <CYT>  
 F:502-782/Domain: protein kinase homology <KIN>

F:510-518/Region: protein kinase ATP-binding motif  
 F:67,95,121,188,202,253,262,281,318,323,338,358,395/Binding site: carbohydrate (asn) (covalent)

F:538/Active site: lys #status predicted  
 F:674/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
 F:785/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 42.8%; Score 1893.5; DB 1; Length 790;  
 Best Local Similarity 48.3%; Pred. No. 2.8e-83;  
 Matches 404; Conservative 116; Mismatches 228; Indels 79; Gaps 21;

QY 7 WH-----GPMARLWGFCLVYVGFMAAFAACPTSCSCASRKWCSDBSPGIVAFPRLEPNS 62  
 DB 12 WHRPA-----GLGLVYTSMLA-----CACASCRCTCCPVGSGIRCTRACTTLTLR 60

Db 12 WHSWAGPGSI-----LAMLLASAGAA-PCPDAC-----CPHGSSGLRC---TRDGA 55  
QY 63 VD-----PENTEIFIANQKLEIINEDVEAYVGLRNLTVDSGLKFAVAKAFKNS 115  
Db 56 LDSLHHLPGAENLTELTYENQOHQHLELRDLRGLGELRNLTIVKSGIRFAPAPDAFHFTP 115  
QY 116 NLQHINFTRNKLTLSLRKHFRLDLSELIVGNPFTCSCDIMWIKTL-QEAKSSPTQDL 174  
Db 116 RLSRLNLSFVALBSLSWKTVOGLSLQELVLSGNPLHSCALRWLQWRWEEBGLGVPQKL 175  
QY 175 YCLNNESSKNTPLANLQIPNCGLPANLAPLTYEBKSLTSGSVAGDPVPMNMYDVGN 234  
Db 176 QCHGQG---PLAMPNASCVPPLTKVQVPNASVDVGDVLLRCQVEGRGLEQAGWILTE 231  
QY 235 LVSKGNMETSHTQG-----SLRTNISSDSGKOISCAENLVGEDSVNLTVHFAPTI 289  
Db 232 L---EQSATVWKSSGLSLGTLTANVSDLRNKLTMCAENDVGRAYSVQVNVSF-PAS 287  
QY 290 TFLSPSTDHWCIPFTVKNPKPALQWIFYNGAILNESKXICTKI--HVTNHTYHGLQ 347  
Db 288 VOLHTAVEMHMSIPFSVDGQAPASLRLWLFNGSVLNETSFIFTEFLPANEYVRHGLR 347  
QY 348 LDNPETHANNGDYTLIAKGEYKDEKQISAHFMGNPGIDGANNYPDYIYEDYGTANDI 407  
Db 348 LNPQTHVNNNGYTLTLANPFGQASIMAFM-----DNPEFENBEDPIPDJNSTS---- 398  
QY 408 GDTNRSNEIPSTDYTKTGREHLSYAVVYVIVASVGRCLVWLFLKTLARHSGKMGKP 467  
Db 399 GDPVEKDETP-FGVSAVVG--LAVFACPLST-----LLVLNKGGRNRFGINRP 447  
QY 468 ASVISNDDSDASPLHHSNPSSESGGPDAVIGMTKIPVLENPQYFGITNSQLKPD 527  
Db 448 A-VLAPEDGLAMSLHFWTLGSSLSPTBGKSGL-----QGHITENPQYFS-----D 493  
QY 528 TFVOHITKRNIVLKREIAGEAFGVFLAECYNLCPEODKIIIVAYKTLKDAASDNARKDPR 587  
Db 494 ACVHHIKRRDVLKMEIAGEAFGVFLAECYNLCPEODKMLVAVKALKEASESARQDFOR 553  
QY 588 EAEILLTLQHEHIVKFGVCVEGDPDLMVPEYMKHGDLNKFIRAHGPPDAVLMAGN--PP 645  
Db 554 EAEILLTLQHOHIVRFGVCTEGRPLMVFYMRHGDINRPLRSHGPDAKLLAGGEDVAP 613  
QY 646 TELTOSQMLHIAQOIAAGMYVLAQHVFHRDLATRNCLVGENLIVKIGDFGMSRDVYSTD 705  
Db 614 GPLGLGQLAVASQVAAQMYVLAGLHVFHRDLATRNCLVGGGLVVKIGDFGMSRDVYSTD 673  
QY 706 YRVVGHITMLPIRMMPPESSIMYRKFTTESDVMSLGVVLMELIFTYGQOPWYQLSNNEVIEC 765  
Db 674 YRVVGHITMLPIRMMPPESSIMYRKFTTESDVMSFGVVLMELIFTYGQOPWYQLSNTEAIDC 733  
QY 766 ITQGRVULQRPCTQOBYTEMLGCMOREPHNRKNIKGIHTLLQNLAKASPVYLDILG 822  
Db 734 ITQGRBELRPACPEVYAIWRCMORPEQQRHSIKDVHARLQALQAAPVYLDVLG 790

Search Completed: February 17, 2005, 00:28:19  
Job time : 49 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 17, 2005, 00:06:11 ; Search time 25 Seconds  
(without alignments)  
1292.980 Million cell updates/sec

Title: US-10-645-546-2  
4419  
Perfect score: 1 MSSWIRHMGPMARLMGFCW.....IHTLLQNLAKSPYLDILG 822  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 154980 seqs, 39324206 residues

Total number of hits satisfying chosen parameters: 154980

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4162.5	94.2	821	1 PCT-US04-42360-2096	Sequence 2096, App
2	2296	52.0	825	1 PCT-US04-23166A-800	Sequence 800, App
3	2296	52.0	825	1 PCT-US04-42360-201	Sequence 201, App
4	2289	51.8	825	1 PCT-US04-23166A-657	Sequence 657, App
5	1901	43.0	799	1 PCT-US04-42360-293	Sequence 293, App
6	1263.5	28.6	337	1 PCT-US04-30360-81	Sequence 81, App1
7	1249	28.3	503	6 US-10-450-763-50636	Sequence 50636, A
8	763.5	17.3	502	1 PCT-US04-23166A-729	Sequence 729, App
9	756	17.1	345	1 PCT-US04-30360-82	Sequence 82, App1
10	722	16.3	985	6 US-10-450-763-47493	Sequence 47493, A
11	679.5	15.4	1367	6 US-10-937-758A-97	Sequence 97, App1
12	676	15.3	1370	6 PCT-US04-42360-862	Sequence 862, App
13	660	14.9	376	1 PCT-US04-30360-83	Sequence 83, App1
14	654	14.8	806	1 PCT-US05-00638-81	Sequence 81, App1
15	634	14.3	370	1 PCT-US04-30360-50	Sequence 50, App1
16	622	14.1	354	1 PCT-US04-30360-93	Sequence 93, App1
17	608.5	13.8	822	8 US-60-647-642-36	Sequence 36, App1
18	601	13.6	306	1 PCT-US04-30360-70	Sequence 70, App1
19	601	13.6	370	6 US-10-450-763-51309	Sequence 51309, A
20	601	13.6	675	6 PCT-US04-30360-29	Sequence 29, App1
21	596.5	13.5	299	1 PCT-US04-42360-604	Sequence 604, App
22	595.5	13.5	806	6 US-10-450-763-51719	Sequence 51719, A
23	590	13.4	1114	1 PCT-US04-42360-604	Sequence 604, App
24	589	13.3	983	1 PCT-US04-23813-4	Sequence 4, App1
25	589	13.3	983	1 PCT-US04-06979-467	Sequence 467, App

26	589	13.3	983	6 US-10-794-514A-467	Sequence 467, App
27	578	13.1	986	8 US-60-646-841-30	Sequence 30, App1
28	578	13.1	997	6 US-10-450-763-36048	Sequence 36048, A
29	578	13.1	1026	6 US-10-450-763-53290	Sequence 53290, A
30	565.5	12.8	485	7 US-11-033-545-525	Sequence 525, App
31	565.5	12.8	803	7 US-11-033-545-340	Sequence 340, App
32	560	12.7	384	1 PCT-US04-30360-68	Sequence 68, App1
33	558	12.6	373	1 PCT-US04-30360-67	Sequence 67, App1
34	557	12.6	310	1 PCT-US04-30360-27	Sequence 27, App1
35	555	12.6	1338	7 US-11-021-951-114	Sequence 114, App
36	555	12.6	1421	6 US-10-450-763-36458	Sequence 36458, A
37	551.5	12.5	1089	6 US-10-450-763-51112	Sequence 51112, A
38	544	12.3	379	1 PCT-US04-30360-45	Sequence 45, App1
39	537	12.2	310	1 PCT-US04-30360-27	Sequence 27, App1
40	537	12.2	388	6 US-10-450-763-50983	Sequence 50983, A
41	536	12.1	312	1 PCT-US04-30360-41	Sequence 41, App1
42	531.5	12.0	987	6 US-10-938-061-100	Sequence 100, App
43	531.5	12.0	987	6 US-10-936-626-100	Sequence 100, App
44	528.5	12.0	343	1 PCT-US04-30360-57	Sequence 57, App1
45	525	11.9	986	6 US-10-938-061-101	Sequence 101, App

ALIGNMENTS

RESULT 1  
PCT-US04-42360-2096  
Sequence 2096, Application PC/TUS0442360  
GENERAL INFORMATION:  
APPLICANT: The General Hospital Corporation doing business as Massachusetts General  
APPLICANT: Hospital / Bayer AG  
TITLE OF INVENTION: Nucleotide sequences involved in pain  
FILE REFERENCE: 17633/2048  
CURRENT APPLICATION NUMBER: PCT/US04/42360  
CURRENT FILING DATE: 2004-12-17  
PRIOR APPLICATION NUMBER: 60/531,341  
PRIOR FILING DATE: 19-Dec-2003  
NUMBER OF SEQ ID NOS: 2587  
SOFTWARE: Perl script  
SEQ ID NO 2096  
LENGTH: 821  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: Refseq / NP\_036863  
DATABASE ENTRY DATE: 2003-10-06  
PCT-US04-42360-2096  
Query Match 94.2%, Score 4162.5; DB 1; Length 821;  
Best Local Similarity 93.6%; Pred. No. 8e-245;  
Matches 769; Conservative 25; Mismatches 27; Indels 1; Gaps 1;  
QY 1 MSSWIRHMGPMARLMGFCWLVGFWPDAFAFCAPTSCCKSASRIWCSDPSPGIVAFPRLEP 60  
DB 1 MSPMPRHMGPMARLMGFCWLVGFWPDAFAFCAPTSCCKSASRIWCSDPSPGIVAFPRLEP 60  
QY 61 NSVDPNTEFFINORLEITINEDDVEAYVGLNLTIVDSGLKFWAHKAKXSNLOHI 120  
DB 61 NSIDPENITELLINORLEITINEDDVEAYVGLNLTIVDSGLKFWAHKAKXSNLOHI 120  
QY 121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMIKTLQBAKSSPDTQDLYCLNES 180  
DB 121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMIKTLQBAKSSPDTQDLYCLNES 180  
QY 121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMIKTLQBAKSSPDTQDLYCLNES 180  
DB 121 NPTNKLTSLSRKAFRRHLDSELIIVGNPFTSCSDIMIKTLQBAKSSPDTQDLYCLNES 180  
QY 181 SKNPLANLQIPNCGLPSPANLAAPNLTVBECKSITLSCSVAGDPVPMNTVDGNLVSKM 240  
DB 181 SKNPLANLQIPNCGLPSPANLAAPNLTVBECKSITLSCSVAGDPVPMNTVDGNLVSKM 240  
QY 181 SKNPLANLQIPNCGLPSPANLAAPNLTVBECKSITLSCSVAGDPVPMNTVDGNLVSKM 240  
DB 181 SKNPLANLQIPNCGLPSPANLAAPNLTVBECKSITLSCSVAGDPVPMNTVDGNLVSKM 240  
QY 241 NETSHTOGLRITITISSDDSGKOISCVAEINLVGDDQSVNLTVAFAPIITLESPTSQH 300  
DB 241 NETSHTOGLRITITISSDDSGKOISCVAEINLVGDDQSVNLTVAFAPIITLESPTSQH 300  
QY 241 NETSHTOGLRITITISSDDSGKOISCVAEINLVGDDQSVNLTVAFAPIITLESPTSQH 300  
DB 241 NETSHTOGLRITITISSDDSGKOISCVAEINLVGDDQSVNLTVAFAPIITLESPTSQH 300  
QY 301 WCIPFTVGNPKPALQWFFYNGAILNESKYICTKIHVTNHTYHGLQLDNFTHMNGDYT 360  
DB 301 WCIPFTVGNPKPALQWFFYNGAILNESKYICTKIHVTNHTYHGLQLDNFTHMNGDYT 360





DATABASE ENTRY DATE: 2003-10-06  
PCT-US04-42360-201

Query Match 52.0%; Score 2296; DB 1; Length 825;  
Best Local Similarity 55.0%; Pred. No. 9,4e-133;  
Matches 468; Conservative 107; Mismatches 206; Indels 70; Gaps 16;

10 PAMARLW-----GFCWL-VGFWRAAFACPTSCKSASRIWCSDPSPGIVAFPLRP--- 60  
7 PAKSFWRIPLGSLVWLDYVG---SVLACPANVCVSKTEINCRPRDDGNL-FPLLEGDS 62  
61 -----NSVD-PENITEIFIANOKRELIINEDVEAYVGLRNLTIVDSGLKFAVAKA 110  
63 GNSNGNASINTDISRNTSIHIENWRGLHTLNAVDMELVGLQKLTIKNSGLRNIQPR 122  
111 FLKNSNLQHINFTNKTLSLRKPRHLDELIVGNPFCSDIMWIKTLQF-AKSSP 169  
123 FAKPHRLRYINLSNRILTLTSWOLFOTLSRELBLEONFPCSCDIRMOMQMOEGEAKL 182  
170 DTODLYCLINSSKNIPLANLQIPNCGLPASANIAPNLVTEBGKSTLSCSVAGDPVPNMY 229  
183 DSQSLYCSADGSQLPFRNINISQCDLPEISVSHNLTVRBGDAVITCNGSGSLPVD 242  
230 WDVGNLVS-----KHNESHHTQSLRITNISSDSGKQISCVANLVGEDQSDVNLTVH 284  
243 WIVTGLQSIHTQTNLMTNTHAINTLVNTVSEDNFTLTCIAENVVGMNASVALTVY 302  
285 FAPITTLSPSTSHHNCIPFTVYGNPKRALQWFTNGAILNESKICTKIHVTHTEYH- 343  
303 YPRVSVLSIEBEVRLERHCIEFVVRGNPPTLHMLNQGOLPRLSKIT-----HMDYQ 354  
344 -----GCLQDNPTNHNNGDYTLIAKNEYGKDEKOISAHFMGWPGLDDGANPNVDPY 397  
355 EGEVSEGLLNKPKPTHYNNNGYTLIAKALSTANQTINGHFLKEP-----PFE--- 402  
398 EDVGTAAIDIGDTTNRSEIPESTDVDTKGRHLSVAVAVVIAVVGFC-LVLMFL- 454  
403 -----STDFPESDSAPTPPTITVTHKREEDTFCVSIAGVLAFA-CVLLVVLFIW 454  
455 KLAHRSKFGMKGPASVISNDDSDASPLHINSNSTPSSSEGGPDAVITGMTKIPVLENP 514  
455 KYGRSRKFGMKGPAAVISGEEDSASPLHINHGITTPSSLDAGPDTVVIQMTRIPIVBNP 514  
515 QYFGITNSQLKPDFTVOHIKRHNIVLKRLEGAGAFKFLACVNLCPREODKILVAVYTL 574  
515 QYFQGNHCKPDTYVQHVKRDIVLKRLEGAGAFKFLACVNLSTFTKDMVLVAVYAL 574  
575 KQASDNARKDFRABELLTNLQHEHIVKFGVCGEGLPILVFEYMKHGDINKFLRAHGP 634  
575 KQPLTAAKDFRABELLTNLQHEHIVKFGVCGEGLPILVFEYMKHGDINKFLRAHGP 634  
635 DAVIABSNP---PTELTQSOMLHIAQOIAAGVYTLASQHFVHRDLATRNCLVGENLIVK 691  
635 DAMILVVGQPRQAKGELISQMLHIASQIASGVYTLASQHFVHRDLATRNCLVGENLIVK 694  
692 IGDGMSRDVYSTDYVYRGHTMLPIRMWPESIMYRKFTTESDWSGIVLWMLFTYTGK 751  
695 IGDGMSRDVYSTDYVYRGHTMLPIRMWPESIMYRKFTTESDWSGIVLWMLFTYTGK 754  
752 QPWTQLSNNEVEICTQGRVLAQRPRTCPQEVYELMCMQREPHMKRIKGIHTLQVLA 811  
755 QPMQOLSTEVIECTQGRVLAQRPRTCPQEVYELMCMQREPHMKRIKGIHTLQVLA 814  
QY 812 KASPVYLDITG 822  
Db 815 KATPIYLDITG 825

RESULT 4  
PCT-US04-23166A-657  
Sequence 657, Application PC/TUS0423166A  
GENERAL INFORMATION:  
APPLICANT: Purdue Pharma L.P.

APPLICANT: Jiefei Tong  
APPLICANT: Gang Jin  
APPLICANT: Rui-Ru Ji  
APPLICANT: Yixun Xu  
APPLICANT: Lillian W. Chiang  
APPLICANT: Daniel J. Lavery  
TITLE OF INVENTION: GENES ASSOCIATED WITH RESPONSES TO NEUROPATHIC PAIN  
FILE REFERENCE: 02755/200M584-M00  
CURRENT APPLICATION NUMBER: PCT/US04/23166A  
CURRENT FILING DATE: 2004-07-06  
PRIOR APPLICATION NUMBER: 60/485,101  
NUMBER OF SEQ ID NOS: 868  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 657  
LENGTH: 825  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US04-23166A-657

Query Match 51.8%; Score 2289; DB 1; Length 825;  
Best Local Similarity 54.4%; Pred. No. 2,5e-131;  
Matches 466; Conservative 111; Mismatches 199; Indels 80; Gaps 17;

10 PAMARLW-----GFCWL-VGFWRAAFACPTSCKSASRIWCSDPSPGIVAFPLRP--- 60  
7 PAKSFWRIPLGSLVWLDYVG---SVLACPANVCVSKTEINCRPRDDGNL-FPLLEGDS 62  
61 -----NSVD-PENITEIFIANOKRELIINEDVEAYVGLRNLTIVDSGLKFAVAKA 110  
63 GNSNGNASINTDISRNTSIHIENWRGLHTLNAVDMELVGLQKLTIKNSGLRNIQPR 122  
111 FLKNSNLQHINFTNKTLSLRKPRHLDELIVGNPFCSDIMWIKTLQF-AKSSP 169  
123 FAKPHRLRYINLSNRILTLTSWOLFOTLSRELBLEONFPCSCDIRMOMQMOEGEAKL 182  
170 DTODLYCLINSSKNIPLANLQIPNCGLPASANIAPNLVTEBGKSTLSCSVAGDPVPNMY 229  
183 NSQNLVCLINDGSQLPFRNINISQCDLPEISVSHNLTVRBGDAVITCNGSGSLPVD 242  
243 WIVTGLQSIHTQTNLMTNTHAINTLVNTVSEDNFTLTCIAENVVGMNASVALTVY 302  
230 WDVGNLVS-----KHNESHHTQSLRITNISSDSGKQISCVANLVGEDQSDVNLTVH 284  
243 WIVTGLQSIHTQTNLMTNTHAINTLVNTVSEDNFTLTCIAENVVGMNASVALTVY 302  
285 FAPITTLSPSTSHHNCIPFTVYGNPKRALQWFTNGAILNESKICTKIHVTHTEYH- 343  
303 YPRVSVLSIEBEVRLERHCIEFVVRGNPPTLHMLNQGOLPRLSKIT-----HVEYQ 354  
344 -----GCLQDNPTNHNNGDYTLIAKNEYGKDEKOISAHFMGWPGLDDGANPNVDP- 394  
355 EGEISSEGLLNKPKPTHYNNNGYTLIAKALSTANQTINGHFLKEP-----PFESTD 405  
395 ---VIEDYGTAAIDIGDTTNRSEIPESTDVDTKGRHLSVAVAVVIAVVGFC-LVLMFL 451  
406 NFILFDEV-----SPTPTITVTHKREEDTFCVSIAGVLAFA-CVLLVVL 449  
452 FLN-KLAHRSKFGMKGPASVISNDDSDASPLHINSNSTPSSSEGGPDAVITGMTKIP 509  
450 FVMINKYGRSKFKFMKGPAAVISGEEDSASPLHINHGITTPSSLDAGPDTVVIQMTRIPI 509  
510 VTEHPQFTNSQLKPDFTVOHIKRHNIVLKRLEGAGAFKFLACVNLCPREODKILV 569  
510 VTEHPQFTNSQLKPDFTVOHIKRHNIVLKRLEGAGAFKFLACVNLSTFTKDMVLVAVY 569  
570 AVKTLKQASDNARKDFRABELLTNLQHEHIVKFGVCGEGLPILVFEYMKHGDINKFL 629  
570 AVKTLKQPLTAAKDFRABELLTNLQHEHIVKFGVCGEGLPILVFEYMKHGDINKFL 629  
630 RAHGPDAVIAEKNP---PTELTQSOMLHIAQOIAAGVYTLASQHFVHRDLATRNCLVGE 686  
630 RAHGPDAVIAEKNP---PTELTQSOMLHIAQOIAAGVYTLASQHFVHRDLATRNCLVGE 689  
687 NLVVKIDGFGMSRDVYSTDYVYRGHTMLPIRMWPESIMYRKFTTESDWSGIVLWML 746

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Db      690 NLAVKIDGFGMSRDVYSTDYRVRGHTMLPIRMMPESIMRKTTSSDVSREVIIMEI 749
Qy      747 FTYGKQPMYQLSNNEVEICTGQVLRPRTCPQEVYELMGQVQREPHMKIKGIIHTL 806
Db      750 FTYGKQPMFQLSNNEVEICTGQVLRPRVCPKQEVYDMLGQVQREPHMKIKGIIHTL 809
Qy      807 LQNLAKASPVYLDILG 822
Db      810 LHALGKATPIYLDILG 825

RESULT 5
PCT-US04-42360-293
; Sequence 293, Application PC/TUS0442360
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 293
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_067600
; DATABASE ENTRY DATE: 2003-10-05
PCT-US04-42360-293

Query Match      43.0%; Score 1901; DB 1; Length 799;
Best Local Similarity 49.0%; Pred. No. 7,66-108;
Matches 407; Conservative 112; Mismatches 254; Indels 58; Gaps 18;

Qy      7 WHGPMARLNGFCMLVVGFMRAAFACPTSCKCSAS-RIMGSDPSPGIAPPRLEP-NSV- 63
Db      12 WHRPA-----GLGLVYLSMLA-----CACASCRETCPPVPSGLRCTRAGTLNLTLR 60
Qy      64 ----DPEVITTEFLANQKRLIINDDVEAYVGLNLTIVDSGLKFAVHAKFLKNSNIQHI 120
Db      61 GLRGAGNLTLYVGNORDLQRLREDFDLQGLSELASTLYVSGLFVAPDAFHFTPRLSHL 120
Qy      121 NPTNKLTSLSRKFRHLDSELLVGNPFTCSDDIMWIKTL-QEASSPTODLYCLNE 179
Db      121 NLSNNALESLSKWTVOGLSLDLDLTLSGNPLHSCALMLQMEQBDLCGYTTQKLGSGS 180
Qy      180 SSKNIPLANLQIPNCGPSSANTAAPNLTVEBKSITLSCSAVAGDPVPMYMDVGNLVSKH 239
Db      181 GDQVLPGLHNH--SCGVPSVKIQMPNDSVEVGDVPLQCVQVGGALQADMLITELSGTA 238
Qy      240 MNEISHHQSGSRIT--NISPDGSGKQISCVAKENYVGBDQDSVNLTPHAPITTYLLEBPTS 297
Db      239 TMKSGDLPSLGLTLVNTSDLNKNKYTCMAENVGABVSQVSVF-PASVHLGAVS 297
Qy      298 DHHHCIPFYVGNKPKALQWYNGAILNESKYICTKI---HTVHTVHGLDLDNPTM 354
Db      298 QHHHCIPFVSVDGQAPSLKRFNFNSVLANETSFTTQPLBSALNTEMRHGLRLNQPTHV 357
Qy      355 NNGDYTLIAKNBYKDEKQISAHFMGPGIDDGANPNYVDIYEDYGTAAIDGTTNRS 414
Db      358 NNGDYTLIAANPYQAAASIMAAFM-----DNPEFNPEDPIPVSPSV-----DTNSTS 407
Qy      415 NEISTVDYTKTGEHLSVYAVNVIA-SVGFCLVLMFLIAKLARSHKFGKGPASVYSN 473
Db      408 R-----DPVEKKDPTPGVSAVAGIAVSALFLSALLVLNKKCGQRSKFGINRPA-VLAP 461
Qy      474 DDGASPLHHSINSNTPPSSSEGGPDVYIIGMTKIPVLENPOYRGITNSQLKPTTFQHI 533

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Db      462 EDGLAMSLHFWTLGSSSLPTBGSGSL-----QGHIMENPOYFS-----DTCVHHI 508
Qy      534 KRNIYVLRKRLGAGAGKVFALACYNLCPEQDKILVAVKTLLKQASDNARQDFRREABLLT 593
Db      509 KRQDIILKMEILGAGAGKVFALACYNLNDQDKLVAVKLAKETSBARQDFRREABLLT 568
Qy      594 NLQHEHLYKRYGVGVGDDPLIMVEYWKIGDLDKPKLRAGHPDVLMAEGN--PPTSLTQS 651
Db      569 MLQHQHLYKRYGVGVGDDPLIMVEYWKIGDLDKPKLRAGHPDVLMAEGN--PPTSLTQS 628
Qy      652 QMLHIAQIAGNYYLASQHFVARDLATRNCLVGENMLVKIDGFGMSRDVYSTDYRYVGG 711
Db      629 QLLAVASQVAAAGNYYLASQHFVARDLATRNCLVGGGLVYVIGDFGMSRDVYSTDYRYVGG 688
Qy      712 HTMLPIRMMPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGQVLR 771
Db      689 RTMLPIRMMPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGQVLR 748
Qy      772 LORPRTCPQEVYELMGQVQREPHMKIKGIIHTLQNLAKASPVYLDILG 822
Db      749 LERRPACPPDVYAIMRGQVQREPHMKIKGIIHTLQNLAKASPVYLDILG 799

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RESULT 6
PCT-US04-30360-81
; Sequence 81, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; PRIOR FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 81
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURES:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-81

```

```

Query Match      28.6%; Score 1263.5; DB 1; Length 337;
Best Local Similarity 68.6%; Pred. No. 1,26-69;
Matches 240; Conservative 37; Mismatches 58; Indels 15; Gaps 3;

Qy      475 DGBASPLHHSINSNTPPSSSEGGPDVYIIGMTKIPVLENPOYRGITNSQLKPTTFQHI 534
Db      1 DGLAMSLHFWTLGSSSLPTBGSGSL-----QGHIMENPOYFS-----DACVHHI 47
Qy      535 RHNIYVLRKRLGAGAGKVFALACYNLCPEQDKILVAVKTLLKQASDNARQDFRREABLLT 594
Db      48 RQDIILKMEILGAGAGKVFALACYNLNDQDKLVAVKLAKETSBARQDFRREABLLT 568
Qy      48 RQDIILKMEILGAGAGKVFALACYNLNDQDKLVAVKLAKETSBARQDFRREABLLT 568
Db      595 LQHEHLYKRYGVGVGDDPLIMVEYWKIGDLDKPKLRAGHPDVLMAEGN--PPTSLTQS 652
Qy      108 LQHQHLYKRYGVGVGDDPLIMVEYWKIGDLDKPKLRAGHPDVLMAEGN--PPTSLTQS 628
Db      653 MLHIAQIAGNYYLASQHFVARDLATRNCLVGENMLVKIDGFGMSRDVYSTDYRYVGG 711
Qy      168 LLAVASQVAAAGNYYLASQHFVARDLATRNCLVGGGLVYVIGDFGMSRDVYSTDYRYVGG 688
Db      713 TMPIRMMPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGQVLR 772
Qy      228 TMPIRMMPESIMRKTTSSDVSLSGLVLMETFTYGKQPMYQLSNNEVEICTGQVLR 749
Db      773 QRPRTCPQEVYELMGQVQREPHMKIKGIIHTLQNLAKASPVYLDILG 822
Qy      288 ERRPACPPDVYAIMRGQVQREPHMKIKGIIHTLQNLAKASPVYLDILG 799

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Best Local Similarity 25.74; Pred. No. 1.4e-33;  
Matches 242; Conservative 128; Mismatches 279; Indels 293; Gaps 41;

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QY 93 LRNLIVDSGLKFAVAKAF--LKSNLQHI-NFTRNKLTSLSRKF-----RHLDSEIL 145
D 402 LKNRLILGEGQLGNGNSFYVLQNLQQLMDWDRNLITLAKGMYFAFNKLCVSELYR 461
QY 146 V-----GNPTSCDIMWIKTLQEAKS-----SPDTODLY 175
D 462 MEEVGTGKRGSKGIDINTRNNGERASCSVDLHFTSTTSKRIITLTHRYRPPDYDLI 521
QY 176 CLNSSLNIPLANQIIR-----CGLPSANLA-----APLTYEEG----- 211
D 522 SFVTVYKEAPPKVNTYDGDACGNSNMWVDVLPPKQDVEPGILLHGLKPTQYAVYV 581
QY 212 KSITLSCSVAGD-----PVNMTWV-----GN 234
D 582 KAVVLT-MVENDHIRGAKSELITRTNASTVPSIPDLVLSANSSSGLIVKKNPSSLRNGN 640
QY 235 L-----VSKHNETS-----HTQSLRI-----TWISSDDSGQ 263
D 641 LSVYIVWQROPQDGYLYRH-NYCSKDKIPIRKYADGTIDIEVTENPKTEVCGGEGPC 699
QY 264 ISC-----VAENLVEDDQSVNLTYH---FAP-----TTFLESPTSDHM 301
D 700 CACPKTEAKQAEKEAEYRKYFENFLNLSIFVRPERKRDVNOVANTTSSRSRYTA 759
QY 302 CIPFTVGNPRLALOW-FYNGAILNESKICTK-----ITHVTH-TEHYGCLQD 349
D 760 ADYVITIDPELETFEYFPFESRVNKKERTVLSNRPFLTVRIDHSCHEAEKLGCC--- 815
QY 350 NPTMNGDVTLLAKNEYGDE-----KOISAHFMGPGIDGANNYPVYI-E-D 399
D 816 ---SASFVFAITMPAE-GADDIPGVTWEPRENSIFLKP---EPENNGILLMYEIK 868
QY 400 YGTAANDI-----GDTTRNSN-----ELPSTDV-----TD-----KT 426
D 869 YGSOVEDQRECVSHQERYKYGAKLNRLNPGNYTARIQATSLSGNSGWTDEVFYVQAKT 928
QY 427 GRE---HLASYAVVIVASVNGFCLLVMLFLKLARHSFGMKGPASVYSNDDASPLHH 483
D 929 GYEFHILIALPVALVILV-GLVIMLYV-----FHR 960
QY 484 ISNGSNTPSSSEGGPDVAVIIGMTKIPVLENPOYFGITNSOLKPTFYOHIKSHNIVAKRE 543
D 961 KRNNR-----LGNGVLYASVNPETFSADVYV-PDEW---EVARREKITMSRE 1004
QY 544 LGEGAFKVFIAECYNLCPEQDKILVAVKTLK-ASDNARKDFRREALLTNLQHEHIVK 602
D 1005 LGQGSFGVYVEGAVAGVVKDEPETRVAIKTVNEAASMRERLEFLNEASVMKEFNGCHVVR 1064
QY 603 FYGCVGEGDPLIMVFYMKIGDILNKLRAHGPDAVLAEGNP---PTELLOSQMLHAQ 659
D 1065 LLAGVSSQGPVLVIMELMTRDLSYRSLEP---MENNPVLAAPSL-SKMIOWAGE 1118
QY 660 IAAQNVYASQHFVHRDLATRNCLVGENLVKIDFGMSRDVYSTDYRYVGGHMLPIRW 719
D 1119 IADGMATLANKKTVHRDLAARNCAVEDFTYKIDFGMTDRIDYETDYRKGGKGLPFRW 1178
QY 720 MPRESIMRKFTTESDVMSLGVLMIEFTYKQOPWYOLSNNEVEICTTQGVLOREPTECP 779
D 1179 MSPESLADGVFTTYSVWMSFQVLMELIATLAEPYQGLSNEGQVAFPMWEGGLDKPNDP 1238
QY 780 QEVYELMLGCGQEPHARKNIKGIIHTLQNLAKASPVYLDL 821
D 1239 DMLELMRMCMQYNPKR-----PSFLEII 1263

```

RESULT 12  
PCT-US04-42360-862  
; Sequence 862; Application PC/TUS0442360  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General

```

; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2048
; CURRENT APPLICATION NUMBER: PCT/US04/42360
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/531,341
; PRIOR FILING DATE: 19-Dec-2003
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 862
; LENGTH: 1370
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_434694
; DATABASE ENTRY DATE: 2003-10-05
PCT-US04-42360-862

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Query Match 15.3%; Score 676; DB 1; Length 1370;

Best Local Similarity 24.4%; Pred. No. 2.3e-33;  
Matches 258; Conservative 134; Mismatches 300; Indels 366; Gaps 45;

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QY 32 CPISCKCSASR-----IWCSDPSRGIYAFRLERNSVDPENITEL-----FINQK 77
D 307 CPISGFINRSTQSMYCIPECBPCPVCGDEBKTKTIDTSVSAQMLQCTTLKGNLLINIR 366
QY 78 RLIEINDEVEAYVG-----LRNLIVDSGLKFAVAKAF--Lk 113
D 367 RGNNT-ASELENFMGLIEVYTGKYNHSHALVSLSLKRLILGEGQLGNGNSFYVL 425
QY 114 NSNLQHI-NFTRNKLTSLSRKF-----RHLDSEILV-----GN 148
D 426 NQNLQQLMDWDRNLITVRSQGMFAFNPKLCVSEIYMEVGTGKRGSKGIDINTRNNGE 485
QY 149 PFTSCDIMWIKTLQEAKS-----SPDTODLYCLNSSLNIPLANQIIR---C 194
D 486 RASGESDVLFTSTTKNRIIITWHRYRPPDYDLISFVTVYKEAPPKVNTYDGDAC 545
QY 195 GLPSANLA-----APNLVEEG-----KSITLSCSVAGD----- 223
D 546 GSNMNMWVDVLPPNKEGEGILLHGLKPTQYAVVYKAVVLT-MVENDHIRGAKSELILY 604
QY 224 ---PVNMTWV-----GNL-----VSKHNE 242
D 605 IRTNASTVPSIPDLVLSANSSSGLIVKKNPPTLPNGLSYIVRWQROPQDGYLYRH-NY 663
QY 243 TS-----HTQSLRI-----TWISSDDSGQISC-----VA 268
D 664 CSKDKIPIRKYADGTIDIEVTENPKTEVCGGKPCACPKTEAKQAEKEAEYRKF 723
QY 269 ENLVGED-----QDSVNLV---VHFAPITTFLESPT 296
D 724 ENFLHNSIFVPRPERRRRDVLQVANTTSSRSRNTVADVTYNTIDPEEFETEPFESRV 783
QY 297 SDHMCIPFTVGNPKPRLQMFYNGAILNESKYICTKIHTVTH-TEHYGCLQDNPTHMN 355
D 784 DNEK-----RVIISNLRFTYXRD-----IHCNHEAEKLGCC-----SAS 819
QY 356 NGDYTLIAKNEYGDE-----KOISAHFMGPGIDGANNYPVYI-E-DYGTAA 405
D 820 NPFVFAITMPAE-GADDIPGVTWEPRENSIFLKP---EPENNGILLMYEIKYGSOVE 875
QY 406 DI-----GDTTRNSN-----ELPSTDV-----TD-----KTGRE--- 429
D 876 DQRECVSROERYKYGAKLNRLNPGNYTARIQATSLSGNSGWTDPVFYVPAKTYNFM 935
QY 430 HLSYAVAVIVASVNGFCLLVMLFLKLARHSKFGMKGPASVYSNDDASAPLHHSNSN 489
D 936 HLIALPVALVILV-GLVIMLYV-----FHRKRNNR 967
QY 490 TPSSSEGGPDVAVIIGMTKIPVLENPOYFGITNSOLKEDTFVQHIKRHNIVLKEGAF 549
D 968 -----LGNGVLYASVNPETFSADVYV-PDEW---EVARREKITMNRLELGGSGF 1011

```





Db 660 WMAPEALFDRVYTHQSDVWSFGVLLMEIFTLGSSPYEGIPVEBELFKLIKESGRMDKQANC 719  
QY 779 POEVEELMTGCMQREPHMRKNKIGIHLLQNLAKASPV-----YLDI 820  
Db 720 THDLYMIMBECMHAAFSQRPTFK---QLVEDLDRLVLTSTDEYIDL 763

## RESULT 15

PCT-US04-30360-50  
; Sequence 50, Application PC/TUS0430360  
; GENERAL INFORMATION:  
; APPLICANT: PLEXIKON, INC.  
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT  
; FILE REFERENCE: 039363-1703  
; CURRENT APPLICATION NUMBER: PCT/US04/30360  
; CURRENT FILING DATE: 2004-09-15  
; PRIOR APPLICATION NUMBER: 60/503,277  
; PRIOR FILING DATE: 2003-09-15  
; NUMBER OF SEQ ID NOS: 167  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 50  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Mammalian  
; OTHER INFORMATION: protein sequence  
PCT-US04-30360-50

Query Match 14.3%; Score 634; DB 1; Length 370;

Best Local Similarity 43.4%; Pred. No. 1.8e-31;  
Matches 131; Conservative 51; Mismatches 110; Indels 10; Gaps 5;

QY 513 NPOYFGITN----SQLKPDFTVCHIKRHNITLKRLEGBGARGKYFLAECTYLCEPDKIL 568  
Db 24 NPEYLSASDVFPCCSVYVPDEM--EVSREKLTLLRELGQSGFQWVYEGNARDIIRGEAETR 81  
QY 569 VAVETLKD-ASDNARKDFHREAEILLTNLQHEHIVKFGVCVEGDPLIMVFEMKGDINK 627  
Db 82 VAVTVNESASLRERIEFLNLSASVWKGFCHHVRLGLGVSKGPTLVVWELMAHGDLKS 141  
QY 628 FLRHGPDAYLMAENPPELTOSQMLHIAQOIAAGVYLAQHFRHDLATRNCLVGEN 687  
Db 142 YLSLRPEAB-NNPGRPP--TLQEMIQMAEIIADGMAYLNAKKFVHRDLAARCMVAHD 198  
QY 688 LTVKIGEGMSRDVYSTDYRVVGHITMLPIRMPPESIMRKFTTESDWSLGIYVMEIF 747  
Db 199 FTVKIGDFGMRDLYETDYRRKGKGLLPVRMMAPESLKDGVFTTSSDMSFGVVLWEIT 258  
QY 748 TYGQPMYQLSNNEVICITQGRVLOBPRTCPQEVVELMLGCMQREPHMRKNKIGIHLL 807  
Db 259 SLAEQPYQGLSNEGVLFVMDGGYLDQPDNCPERVTLDMRCWQFNPMMRPTFLEIVNL 318  
QY 808 QN 809  
Db 319 KD 320

Search completed: February 17, 2005, 00:18:59  
Job time : 29 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: February 18, 2005, 00:12:45 ; Search time 16333.1 Seconds  
(without alignments)  
10997.536 Million cell updates/sec

Title: US-10-645-546-1  
Perfect score: 3707  
Sequence: 1 ccccatcgcacatcaacaa.....gtagagagcaagatggctc 3707

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : GenBmb1.\*  
1: gb Da:\*  
2: gb Hg:\*  
3: gb In:\*  
4: gb Om:\*  
5: gb Ov:\*  
6: gb Pat:\*  
7: gb Ph:\*  
8: gb Pl:\*  
9: gb Pr:\*  
10: gb To:\*  
11: gb Sts:\*  
12: gb Sy:\*  
13: gb Un:\*  
14: gb Vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3707	100.0	3707	6	I35538 Sequence 1
2	3707	100.0	3707	9	HSU12140 Human tyros
3	3649	98.4	4057	9	AR410899 Homo sapi
4	3156.6	85.2	3194	6	AR063152 Sequence
5	3156.6	85.2	3194	6	AR071348 Sequence
6	3156.6	85.2	3194	6	AR119334 Sequence
7	3156.6	85.2	3194	6	AR119334 Sequence
8	2610	70.4	2610	9	S76473 Human
9	2519.4	68.0	3060	6	AR400441 Homo sapi
10	2519.4	68.0	3060	6	AR069424 Sequence
11	2264.2	61.1	4757	6	AR168009 Sequence
12	2264.2	61.1	4757	6	AX683038 Sequence
13	2193.4	59.2	4351	10	MSTRKB1
14	1962	52.9	2463	6	I40971 Sequence 1
15	1950	52.6	1961	6	CQ723233 Sequence
16	1936	52.2	8192	9	AF410900 Homo sapi
17	1878	50.7	8240	9	AF410901 Homo sapi
18	1731.2	46.7	2328	9	BC031835 Homo sapi
19	1604.6	43.3	3201	5	GGTRKBRFL X77251 G.gallus tr

20	1519.8	41.0	2697	5	GDTRKB	X74109 G.domesticu
21	1484.2	40.0	1870	6	AR063153	AR063153 Sequence
22	1484.2	40.0	1870	6	AR071349	AR071349 Sequence
23	1484.2	40.0	1870	6	AR119335	AR119335 Sequence
24	1484.2	40.0	1870	9	S76474	S76474 ttrk (alter
25	1482	40.0	6679	9	AF508964	AF508964 Homo sapi
26	1480.4	39.9	2224	6	AX331537	AX331537 Sequence
27	1480.4	39.9	2224	6	HSTRKBR	X75958 H.sapiens t
28	1271.4	34.3	2393	5	AY679520	AY679520 Taeniolopyg
29	1152.8	31.1	3444	5	XLU39670	XLU39670 Xenopus lae
30	1134.6	30.6	2279	10	BC052014	BC052014 Mus muscu
31	1133.2	30.6	2249	10	RATRKX2	M55222 Rat neural
32	1133.2	30.6	3960	10	AY265419	AY265419 Rattus no
33	1129.6	30.5	3414	5	XLU39671	U95671 Xenopus lae
34	1118	30.2	3991	10	RATRKX3	M55223 Rat neural
35	1085	29.3	2484	10	MSTRKB	M33385 Mouse tyros
36	1063.2	28.7	171629	2	AL445532	AL445532 Human DNA
37	1063.2	28.7	188676	2	AC024515	AC024515 Homo sapi
38	978	26.4	1057	6	CQ723929	CQ723929 Sequence
39	853	23.0	853	11	G15862	G15862 human STS C
40	797.6	21.5	2313	9	AB066522	AB066522 Macaca fa
41	789.4	21.3	2625	5	XLU39672	U95672 Xenopus lae
42	690	18.6	1910	5	GGTRKBT	X77252 G.gallus tr
43	686.8	18.5	2478	10	AY336094	AY336094 Mus muscu
44	681.8	18.4	2940	6	AR069425	AR069425 Sequence
45	681.8	18.4	2940	6	AR168010	AR168010 Sequence

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
I35538	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
LOCUS	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
DEFINITION	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
ACCESSION	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
VERSION	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
KEYWORDS	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
SOURCE	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
ORGANISM	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
REFERENCE	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
AUTHORS	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
TITLE	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
JOURNAL	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
FEATURES	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
source	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
ORIGIN	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
Query Match	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
Best local Similarity	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
Matches 3707;	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
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Mismatches	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
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Gaps	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;
0;	Sequence 1	from patent US 5601820.	I35538	1	GI:2087389	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 3707)	Brodeur/G.M. and Nakagawara,A.	Compositions and methods of making and using human full length	Patent: US 5601820-A, 11-FEB-1997;	Patent: US 5601820-A, 11-FEB-1997;

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 Nycum, L. M., Bigel, J. A. and Brodeur, G. M.  
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 kinase receptor gene (NTRK2)  
 Genomics 25 (2), 538-546 (1995)  
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 Direct Submission  
 Submitted (08-JUL-1994) Akira Nakagawara, Division of Oncology,  
 Children's Hospital of Philadelphia, 34th & Civic Center Blvd.,  
 Philadelphia, PA 19104, USA  
 JOURNAL  
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
AUTHORS Stoilov P., Castren, E. and Stamm, S.  
TITLE Analysis of the human TrkB gene genomic organization reveals novel  
JOURNAL TrkB isoforms, unusual gene length, and splicing mechanism  
MEDLINE 21656983  
PUBMED 11798182  
REFERENCE  
2. (bases 1 to 4057)  
Stoilov P.G., Castren, E. and Stamm, S.  
TITLE Direct Submission  
JOURNAL Submitted (16-APR-2001) Institute of Biochemistry, FAU Erlangen,  
Faculty of Medicine, Fahrstrasse 17, Erlangen 91054, Germany  
FEATURES  
Location/Qualifiers

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ORIGIN

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ORGANISM Unknown.  
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ORIGIN

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DB 1034 GAAAGCAACCCCAACCAACGAGCTTCAAGTGTCTTAACCGGCAATATTGAATGATC 1093  
QY 1332 CAATATCACTGTATCTTAATATCATGTTACCAATTCACAGGAGTACAGGCTGCTCCA 1391  
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QY 1392 GCTGATTAATCCCACTCACTGAAACAAATGGGACTACACTTAATAGCCAAAGATGATA 1451  
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QY	2392	ACTGACGAGTCGCGAGATGCTGCAATATAGCCACGACAGATATGCGCGGCGCATATGCTACCT	2351
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Db	2174	CTTGCTGGTGAATAATCGGGGACTTTTGGGATATGCCCGGGAGCGTGTATACACTGTACTATA	22333
QY	2472	CAGGGTCGGTGGCCACAAATATGCTGCCATTTCGCTGATATGCTCAGAGACATCATATCTA	25311
Db	2234	CAGGGTCGGTGGCCACAAATATGCTGCCATTTCGCTGATATGCTCAGAGACATCATATCTA	22933
QY	2532	CAGAAATATCAAGAGAAAGCGAGCTGTGAGACCTTGGGGGTCTGTTGTGGAGATTTT	2591
Db	2294	CAGAAATATCAAGAGAAAGCGAGCTGTGAGACCTTGGGGGTCTGTTGTGGAGATTTT	23533
QY	2592	CACCTATATGGCAAAACAGCCCTGTGTACACACTGTCAAAACAATGAGGTGATATGATGTATAC	2651
Db	2354	CACCTATATGGCAAAACAGCCCTGTGTACACACTGTGTCAAAACAATGAGGTGATATGATGTATAC	24133
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Db	2414	TCAGGGCCGAGATCTCTGACAGCAACCCCGACGTCGCCCGAGAGAGGTATATGAGCTGATGCT	24733
QY	2712	GGGGTGCTGGCAGCGAGAGCCCAATGAGGAAAGACATCAAGGGCATTCATACCTCTCT	27711
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QY	2772	TCAGAACCTTGGCCAAAGGATCTCCGGTCTACCTGGAATTTAGGCTATGGGCCCTTTTCC	28311
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QY	2832	CCAGACGCAATCCTTCCCAACGATCTCTCCAGACGGGCGGAGAGATGAAACATCTTTTAC	2891
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QY	2892	TGCGGCTGGAAGGCGACCAAGCTGCTCTCTTCACTCTGACAGTATTAATCAATCAAGAATC	2951
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Db	2774	TTTTTGGATATCTCTTCTCTCTTCCATCTCCCTGTGTGTCTCTTTCTTTTCTT	28333
QY	3072	AAATTTTCTTTTCTCTTTTCTTGGCTTCCCGCTTCAAGATTTTCAACCTTTCTT	31311
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QY	3132	TGAATCAATCTGGCTTGTGCAATTAATCTGTGACATAGACAAAGGCTTTACAAACG	3191
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QY	3192	TAAATTTGTTAATATCAGACACATCTCAATTTGCCACCAACAATTAACATGCTGTGTGT	3251
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QY	3252	TTTCTGCGCTTGTATGTCGATGAGAAAAAAGGAAAAACAAATATTCACTTAACTTGTCTC	3311
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QY	3312	ACTTCGTGTCGATGAGATATTCGAGAGTTTCTATGGAATTCATCTTATTTATTTATTTAT	3371
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QY	3372	TACTGTTCTTATTTGTTTTTGGATGGCTTTAGCCTGTGTATATAAAGAAAA	3422
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DEFINITION	Sequence 1 from patent US 5910574.		linear
ACCESSION	AR071348		
VERSION	AR071348.1	GI:7222236	
KEYWORDS			
SOURCE			
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3194)		
AUTHORS	Presta,L.G., Shelton,D.L. and Ufreic,R.		
TITLE	Human trk receptors and neurotrophic factor inhibitors		
JOURNAL	Patent: US 5910574-A 1 08-JUN-1999;		
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ORIGIN			
Query Match	85.2%; Score 3156.6; DB 6; Length 3194;		
Best Local Similarity	99.7%; Pred. No. 0;		
Matches 3162; Conservative	0; Mismatches 9; Indels 0; Gaps 0;		
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Db	14	AAGAAAGCCGCAAGCGCAAGCGGAGCGCTCCCGCACGGGTGGGGAAAGCGCGCGTCACA	73
QY	312	GCGCGGGGACAGGCACTCGGGCTGGCACTGCGCTGTAGGAGATGTCCTCGATATPAGGTG	371
Db	74	GCGCGGGGACAGGCACTCGGGCTGGCACTGCGCTGTAGGAGATGTCCTCGATATPAGGTG	133
QY	372	GCATGGAACCGGCACATGCGCGCGCTCTGCGGCTTGTGCTGCTGTGTTGTGGCCTTCTGGAG	431
Db	134	GCATGGAACCGGCACATGCGCGCGCTCTGCGGCTTGTGCTGCTGTGTTGTGGCCTTCTGGAG	193
QY	432	GGCGGCTTTGGCGCTGTGCCACGTCCTCGCAATTCAGAGCCCTCGGGAATCTGTGACGGA	491
Db	194	GGCGGCTTTGGCGCTGTGCCACGTCCTCGCAATTCAGAGCCCTCGGGAATCTGTGACGGA	253
QY	492	CCCTTCTCTGGGACATCGTGGCATTTCCGAGATTGGAGCGCTAAACAGTGTAGATCTTGAGAA	551
Db	254	CCCTTCTCTGGGACATCGTGGCATTTCCGAGATTGGAGCGCTAAACAGTGTAGATCTTGAGAA	313
QY	552	CATCACCGAAATTTTCATCGCAAAACGAGAAAAGTTAGAAATCATCAACGAAGATGATGT	611
Db	314	CATCACCGAAATTTTCATCGCAAAACGAGAAAAGTTAGAAATCATCAACGAAGATGATGT	373
QY	612	TGAAGCTTATGTGGGACATGAGAAATCTGACAATTGTGATTTCTGGAATTAATAATTTGTGGC	671
Db	374	TGAAGCTTATGTGGGACATGAGAAATCTGACAATTGTGATTTCTGGAATTAATAATTTGTGGC	433
QY	672	TCATTAAGCAATTTCTGAAAAACAGCAACTTCAGACACATCAATTTTACCCGAAACAACT	731
Db	434	TCATTAAGCAATTTCTGAAAAACAGCAACTTCAGACACATCAATTTTACCCGAAACAACT	493
QY	732	GACGAGTTTGTCTTAGAAAAACATTTTCGGTACCTTGACTTGTCTGAACTGATCTCTGTGTGG	791
Db	494	GACGAGTTTGTCTTAGAAAAACATTTTCGGTACCTTGACTTGTCTGAACTGATCTCTGTGTGG	553



QY 792 CAATCCATTACATGCTCTGTGACATTATGTGATCAAGACTCTCCAAAGGCTAATC 851  
Db 554 CAATCCATTACATGCTCTGTGACATTATGTGATCAAGACTCTCCAAAGGCTAATC 613  
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QY 1752 AGCTTCCTGTTATCAGCAATGATGATGACTGTGCAAGCCCACTCATCATCTCCAAATGG 1811  
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QY 2232 GTTCTCAAGGCGACCGCCCTGATGCGGTGATGAGTGGAGGCGAACCCGCCAAGGA 2291  
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Oy	3192	TAAATTTGTTATATACGACGACACTCCAGTTGGCCACACAACTAACATGCCCTGTTGT	3251
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Oy	3252	ATTCTCGCTTTGATGTGATGAGAAAAAGGAAAAACAATATTCTACTTAACTTGTCTC	3311
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Db	3074	ACTTCTGCTGATACAGATATCGAGAGTTCTATGATTTCACTTCTATTTATTTATATAT	3133
Oy	3372	TACTGTTCTTATGTTTTTGGATGGCTTAACCTGTGTATATAAAAAAGAAA	3432
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DEFINITION	Sequence 1 from patent US 6153189.				
ACCESSION	AR119334				
VERSION	AR119334.1	GI:14102033			
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ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 3194)				
TITLE	Presta, L.G., Shelton, D.L. and Ufer, R.				
JOURNAL	Human TRK receptors and neurotrophic factor inhibitors				
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OY	612	TGAAGCTTATGTGGGACTGAGAAATCTGACAAATGTGGATTCTGCAATTAATTTGTGGC	671
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OY	672	TCATPAAGCAATTTCTGAAAAACAGAACCTGGACACATCAATTTTACCAGAAACAACT	731
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OY	732	GACGAGTTTGTCTAGAAACATTTCCGCTCACTTGACTTGTCTGAACCTGATCTCGTGGG	791
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OY	792	CAATCCATTTACATGCTCTGTGTGACATTAATGTGATCAAGACTCTCCAAAGGCTAAATC	851
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OY	852	CAGTCCAGACCTCAGAGATTTGTACTCCCTGAAATGAAGAAGCAAGAAATATTTCCCTGGC	911
Db	614	CAGTCCAGACCTCAGAGATTTGTACTCCCTGAAATGAAGAAGCAAGAAATATTTCCCTGGC	673
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OY	972	TGTGAGAGAAAGAAAGTCTATCACATTAATCTGTAGTGTGGCAGAGTATCGGATTCCTAA	1031
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## KEYWORDS

SOURCE  
 ORGANISM

Homo sapiens (human)  
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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JOURNAL  
 MEDLINE  
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VERSION  
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Wu, J., Zhang, B., Zhou, Y., Peng, X., Yuan, J. and Qiang, B.  
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Basic Medical Science, Chinese Academy of Medical Sciences and  
Peking Union Medical College, 5 Dong Dan San Tiao, Beijing 100005,  
P. R. China

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ORIGIN

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DB 361 GATGTGAAGCTTATGTGGGAGTGAATACTGCAATTTGGATTCTGGATTAAATTT 420

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DB 1381 ACCGCTGGAGAACATCTCTGGTGTATGCTGTGGTGTGATTCGCTGTGGTGGATTT 1440

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VERSION AR069424.1 GI:7220312  
KEYWORDS  
SOURCE .  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3060)  
AUTHORS Godowaki, P.J., Mark, M.R., Sadick, M.D., Shelton, D.L. and  
Mong, W. Lee, Tan.  
TITLE Kinase receptor activation assay  
JOURNAL Patent: US 5891650-A 6 06-APR-1999;  
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 Godowski, P.J., Marx, M.R., Sadick, M. Daniel, and Wong, W. Lee. Tan.  
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RESULT 11  
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LOCUS AX683038 4757 bp DNA linear PAT 29-MAR-2003  
DEFINITION Sequence 12 from Patent EP1297944.  
ACCESSION AX683038  
VERSION AX683038.1 GI:29370110  
KEYWORDS Rattus norvegicus (Norway rat)



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RESULT 12  
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LOCUS RATRKBI 4757 bp mRNA, complete  
DEFINITION Rat neural receptor protein-tyrosine kinase (trkb) mRNA, complete  
cd8.  
ACCESSION M55291.1 GI:207473  
VERSION M55291.1 GI:207473  
KEYWORDS neural receptor protein-tyrosine kinase.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 4757)  
Middelman, D.S., Lindberg, R.A. and Hunter, T.  
trkb, a neural receptor protein-tyrosine kinase: evidence for a  
full-length and two truncated receptors  
Mol. Cell. Biol. 11 (1), 143-153 (1991)  
JOURNAL 91094826  
MEDLINE 1846020  
PUBMED  
Original source text: Rat (Sprague-Dawley) adult cerebellum, cDNA  
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Beet Local Similarity 79.5%; Pred. No. 0; Mismatches 618; Indels 134; Gaps 15;
Matches 2919; Conservative 0;

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Qy   485  GCAAGGACCTTCTCTGAGCATGTGAGCATTTCCAGATTGGAGCTTAAAGTGTAGATC 544
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Qy	3128	CTTTTGAATCAATCTGGCTCTTGCAATATTAATCTGTGATGACAAAGGCTTTAA	3187
Dp	3471	CTCCCTGACCAATCTGGGCTCTGTACTCTTAATCACTGATCATGTAGACAAAGGCTTTAA	3530
Qy	3188	AACGTAATTTGTATATCAGACGACACTCCAGTTTGGCCACCAACATTAACAATAGCCTTG	3247
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Qy	3248	TTGTATTCCTGCCCTTGTGATGTGATGAAAAAAGGAAAAAATAATTT-----TCACTT	3301
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[illegible][illegible]

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LOCUS  
DEFINITION Sequence 1 from patent US 5622862.  
ACCESSION 140971

VERSION 140971.1 GI:2082451  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2463)  
AUTHORS Squitro,S.P., Glass,D., Aldrich,T.H., Distefano,P., Stitt,T.,  
Furch,M.E. and Yancopoulos,G.D.  
TITLE Assay systems for erbB neurotrophin activity  
JOURNAL Patent: US 5622862-A 1 22-Apr-1997;  
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Db 1 ATGTGCGCCCTGGCTGAAGTGCATGAGACCCGCGCATGGGCGGCTCTGGGGCTTAATGCTGG 60  
QY 412 CTGGTTGTGGGCTTCTGGAGGGCGGCTTTCGCTGTCCTGCAAGTCTGCAAAATGCAATGCC 471  
Db 61 CTGGTCTTGGGCTTCTGGAGGGCGGCTTTCGCTGTCCTGCGCGAGTCTGCAAAATGCAATGCC 120  
QY 472 TCTGGAATCTGGTGCAGGACCCCTTCTCTGGCAATCTGGCAATTTCCGAAATGGAGGCT 531  
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QY 532 AACGATGAATCTCTGAAGATCAACGGAATTTTCAATCCGAAACCGAAAGGTTGAA 591  
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Db	1918	GAGGGTAAACCCGCCCAACGAGCTGACGAGATGCGAGATGTGCAATCGCTCAGCAAAATC	1977
QY	2332	GCOCGCGGCAATGTCATCTACCTGCGCTCCACAGACTTCGTGCACCGCGATTTGGGCCACCAAG	2391
Db	1978	GCACGAGGTATGTCTTACCTGCGCTCCACAACTTTGTGACCGGTGACTGTGGCCACCCGG	2037
QY	2392	AAGTGCCTGTGTGCGGGAGAACTTGCTGTGTGAAAAATCGGGGACTTTGGGATGTGCCGGGAC	2451
Db	2038	AACTGCTCGTGTGGGAGAGAACCTGCTGTGTGAAAAATTTGGGACTTTGGGATGTGCCGAGAT	2097
QY	2452	GTGTACAGCACTGACTACTACAGGGTGTGTGGCCACACATATGTCGCCCATTCGCTGATG	2511
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QY	2512	CCTCCAGAGACATCATGTATACAGGAAATTCACACGAAATCGAGATGTGTGAGCTGTGGG	2571
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QY	2572	GTCTGTGTGTGGGAGATTTTCACTATGTGGCAAAAGCCCTGTGTACCACTGTCAAACAAT	2631
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Db	2278	GAGGTGATAGAGTGTATCACTACGAGGAGAAAGTCTTCAACGCGCTGTGAACTGTGCCAG	2337
QY	2692	GAGGTGTATAGACTGATCTGTGGGGGTGTGGGACGAGACCCCAATGAGGAGAAACATC	2751
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QY	2752	AAGGCACTCATACCCCTCTTCAGAACTTGGCCAAAGGCACTTCGAGTCTACCTGAGCAAT	2811
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DEFINITION	Sequence 9147 from Patent WO02068579.		
ACCESSION	CQ723213		
VERSION	CQ723213.1	GI:42284070	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.		
TITLE	Ki67s, such as nucleic acid arrays, comprising a majority of		
	humanexons or transcripts, for detecting expression and other uses		
JOURNAL	Patent; WO 02068579-A 9147 06-SEP-2002;		
FEATURES	PE Corporation (NY) (US)		
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ORIGIN	/db_xref="taxon:9606"		

Query Match	52.6%;	Score 1950;	DB 6;	Length 1961;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1961; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

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Qy	1986	GGAAGAGACCTTTGAAAAGTGTCTTAGCTGAATGCTATACTCTGTCCCTGAGCAGAA	2045
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Qy	2166	CGTCTGCGTGAAGGGCCACCCCTCATCATGCTTTTGAAGTACATGAAGCATGGGGACT	2225
Db	421	CGTCTGCGTGAAGGGCCACCCCTCATCATGCTTTTGAAGTACATGAAGCATGGGGACT	480
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Qy	2286	CACGGAATGACGCAATGTCGCAATATAGCCACGAAATGCCCGCGGGCAATGCT	2345
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Qy	2706	GATGCTGGGGGTGCTGGCAGCGAGAGCCCAATAGGAAGAACTCAAGGGCATCCATAC	2765
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Qy	2766	CCTCCTTGAGAACTTGGCCAGAGGATCTCCGGTCTACCTGGAATTTAGGCTTAGGGCC	2825
Db	1021	CCTCCTTGAGAACTTGGCCAGAGGATCTCCGGTCTACCTGGAATTTAGGCTTAGGGCC	1080
Qy	2826	TTTTTCCCAAGCGATCTTCCCAAGTACTCTCAAGCGGCTGAGAGATGAATCT	2885

Db 1081 TTTTCCCAAGCGATCTTCCCAAGCTACTCTCAGACGGGCTGAGAGATGAACATCT 1140  
Qy 2886 TTTTACTGCGCTGAGAGCCACAAAGCTGCTCTCTTCACTGTGACAGATTTAACATCAA 2945  
Db 1141 TTTTACTGCGCTGAGAGCCACAAAGCTGCTCTCTTCACTGTGACAGATTTAACATCAA 1200  
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Db 1201 AGACTCCGAGAAAGCTCTGAGAGGAGAGAGTGTACTTTCTTCAATCATTAGACAGATATT 1260  
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Qy 3126 TTTTAAATTTCTTTTCTCTCTTTTCTTGTGCTTCCCTGCTTCAAGATTTTACCT 3185  
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Db 1500 TGTGTATTCCTGCTTTGATGTGATGATAAAGGAAACAAATATTCACTTAAC 1559  
Qy 3306 TTTGTCACTTCTGCTGATACAGATATCGAGTTTCTATGATTCATTTTATTTAT 3365  
Db 1560 TTTGTCACTTCTGCTGATACAGATATCGAGTTTCTATGATTCATTTTATTTAT 1619  
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Db 1620 TATTATTACTGTTCTTATGTTTGTGATGCTTAAGCTGTATATAAAGAAACTT 1679  
Qy 3426 GTGTTCAATCTGTAGAGCTTATCTATGAGAGATTAAACGAGAGAAAGAAATTTA 3485  
Db 1680 GTGTTCAATCTGTAGAGCTTATCTATGAGAGATTAAACGAGAGAAAGAAATTTA 1739  
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Qy 3606 GGACCTTTCTGAGAGATTAAGAAAGACTACTGGCTCTGTGCAATGATATTTTCCCA 3665  
Db 1860 GGACCTTTCTGAGAGATTAAGAAAGACTACTGGCTCTGTGCAATGATATTTTCCCA 1919  
Qy 3666 TCACCAGAAATGATAGCTGCAATGAGAGCAAAAGATGCTT 3707  
Db 1920 TCACCAGAAATGATAGCTGCAATGAGAGCAAAAGATGCTT 1961

Search completed: February 18, 2005, 11:46:22  
Job time : 16377.1 secs

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XX 29-JUN-1995; 95MO-US008180.
XX 07-JUL-1994; 94US-00271454.
XX (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX Brodeur GM, Nakagawara A;
XX WPI; 1996-097583/10.
XX Nucleic acid encoding human neurotrophic factor receptor. TRK-B - used to
XX develop primers and antibodies for use in assays to determine
XX aggressiveness of neuroblastoma tumours.
XX Claim 1; Page 37-39; sipp; English.
XX The cDNA encodes a full length human neurotrophic factor receptor TRK-B.
XX TRK-B is a receptor for brain-derived neurotrophic factor but it also
XX binds neurotrophin-3 and -4/5. The cDNA can be used to express the full
XX length protein and to design primers for detection of the presence of TRK
XX -B transcripts in cells. Antisense oligonucleotides can be used to
XX inhibit the expression of TRK-B in neuroblastomas
XX
XX Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;
Query Match 100.0%; Score 3707; DB 2; Length 3707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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D 1 CCCCATTGCGATTAACAAGGATCTGCGCCGAGAGTCCCGGACGCCCGGTGG 60
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D 61 TGCCCGCGCGCCGCGCATGACGACGCGCCGCGGAGCTCCGAGACGGGTAGCG 120
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D 181 CTCTTCCTCCGACCAAGCTCTGATTAAGTGAATCGGCAAGCCCGCAACAAGC 240
QY 241 ACCGAGAGTTAAGAGACGCGCAAGGAGGCTCCCGGCAAGGAGGAGGAG 300
D 241 ACCGAGAGTTAAGAGACGCGCAAGGAGGCTCCCGGCAAGGAGGAGGAGGAG 300
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D 301 CGGCGGATGACGCGGAGGACGAGCACTCGGCTGAGCACTGTGATGAGATGTCTCC 360
QY 361 TGAATTAAGTGGCATGACCCGCAATGAGCGGCTCTGGGGCTTCTGTGGTGTG 420
D 361 TGAATTAAGTGGCATGACCCGCAATGAGCGGCTCTGGGGCTTCTGTGGTGTG 420
QY 421 GGGCTTGAAGAGGCGGCTTGGCTGCTCCAGCTCTGCAAAATGCAATGCTCTCGAATC 480
D 421 GGGCTTGAAGAGGCGGCTTGGCTGCTCCAGCTCTGCAAAATGCAATGCTCTCGAATC 480
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D 481 TGGTGAAGCAACCTTCTCTGAGCATGATGAGATTTCCGAGATTGAGACCTTAACAGTGA 540
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RESULT 2  
AAD45786  
ID AAD45786 standard; DNA; 3707 BP.  
XX AAD45786;  
XX  
XX  
XX 27-DEC-2002 (first entry)  
XX  
XX Human TrkB DNA.  
XX Human; neurodegenerative disorder; neurodevelopmental disorder; TrkB;  
XX TrkB; Alzheimer's disease; AD; amyotrophic lateral sclerosis; ALS; PD;  
XX Parkinson's disease; Huntington's disease; HD; Lou Gehrig's disease;

KM diabetic peripheral neuropathy; Down's syndrome; DS; neuroprotective;  
KM gene therapy; anticonvulsant; cerebroprotective; neurotropic; gene; ds.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH Key 352..2820  
FT CDS /\*tag= #  
FT /product= "Human TrkB protein"  
TN MO200267858-A2.  
PN 06-SBP-2002.  
PD 22-FEB-2002; 2002MO-US005151.  
PF 22-FEB-2001; 2001US-0270553P.  
PR (UOMA-) UNIV MARYLAND BALTIMORE.  
PA Krueger BK, Kingsbury TJ, Bambrick LJ, Dorsey SG,  
PI MPI; 2002-698627/75.  
DR P-PSDB; AAE27931.  
XX Treating and/or preventing neurodegenerative and neurodevelopmental  
PT disorders such as Alzheimer's, Parkinson's and Huntington's diseases by  
PT altering the ratio of amount of full-length and truncated TrkB or TrkC  
PT polypeptides.  
XX Disclosure; Page 54-56; 96pp; English.  
XX The present invention relates to a method of treating neurodegenerative  
CC or neurodevelopmental disorders in a mammal which involves administering  
CC an isolated nucleic acid encoding a full-length TrkB or TrkC or their  
CC mutant, variant, homologue or fragment or an anti-sense RNA for truncated  
CC TrkB or TrkC isoforms, where they increase the amount of full-length TrkB  
CC or TrkC or decrease the amount of truncated TrkB or TrkC in treated  
CC neurons. The methods and compositions of the invention are useful for  
CC treating or preventing neurodegenerative or neurodevelopmental disorders  
CC such as Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's  
CC disease (HD), amyotrophic lateral sclerosis (ALS; Lou Gehrig's disease),  
CC diabetic peripheral neuropathy, the adverse complications of Down's  
CC syndrome (DS) and other types of peripheral neuropathy. Sequences of the  
CC invention are also used in gene therapy. The present sequence is human  
CC TrkB DNA  
XX  
SQ Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;  
Query Match 100.0%; Score 3707; DB 6; Length 3707;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 121 CCCCCTGTAAAGCGGTTGCTATGCGCGGAGCACTGTAACTCTGCGCGCTGCGGAA 180  
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QY 181 CTCTTCGTCGCGGACGAGCTGATGCTGATGCTGCTGCGGAGCACTGCTGCGGAGCA 240  
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Qy 1441 AAGATGATATGGGAAGATGAGAAAGATTTCTGCTCACTTCATGGGCTGGCTGGA 1500  
Db 1441 AAGATGATATGGGAAGATGAGAAAGATTTCTGCTCACTTCATGGGCTGGCTGGA 1500  
Qy 1501 ATTGACATATGGTGAACCCAAATTAATCTGATGTAATTAATTAATGAAGTATGAAGTGA 1560  
Db 1501 ATTGACATATGGTGAACCCAAATTAATCTGATGTAATTAATTAATGAAGTATGAAGTGA 1560  
Qy 1561 GCGAATGACATCGGGGACACCAAGAAATGAATGAAATCCCTTCCACAGAGCTCACT 1620  
Db 1561 GCGAATGACATCGGGGACACCAAGAAATGAATGAAATCCCTTCCACAGAGCTCACT 1620  
Qy 1621 GATTAATACCGGTGCGGGAACATCTCTCGGTCTATGCTGCTGATGCTGATGCTGCTG 1680  
Db 1621 GATTAATACCGGTGCGGGAACATCTCTCGGTCTATGCTGCTGATGCTGATGCTGCTG 1680  
Qy 1681 GGATTTTGGCTTTTGTATGCTGTTTCTGCTTAAGTTGGAAGACACTCCAGTTTGGC 1740  
Db 1681 GGATTTTGGCTTTTGTATGCTGTTTCTGCTTAAGTTGGAAGACACTCCAGTTTGGC 1740  
Qy 1741 ATGAAAGGCCAGCTCTCGTTATGACAAATGATGATGATCTTGGCAGCCCACTCCATAC 1800  
Db 1741 ATGAAAGGCCAGCTCTCGTTATGACAAATGATGATGATCTTGGCAGCCCACTCCATAC 1800  
Qy 1801 ATCTCCAAATGGAGATACATCCACATCTTCTTCGGAAGTGGCCGAGAGCTGTCAATTT 1860  
Db 1801 ATCTCCAAATGGAGATACATCCACATCTTCTTCGGAAGTGGCCGAGAGCTGTCAATTT 1860  
Qy 1861 GGAATGACCAAGATCCCTGTATGAAATATCCCGAGTACTTGGCATCAACCAAGTGA 1920  
Db 1861 GGAATGACCAAGATCCCTGTATGAAATATCCCGAGTACTTGGCATCAACCAAGTGA 1920  
Qy 1921 CTCAAGCCAGACATTTGTTCAAGCAATCAAGGACATTAATTTCTGAAAGGAG 1980  
Db 1921 CTCAAGCCAGACATTTGTTCAAGCAATCAAGGACATTAATTTCTGAAAGGAG 1980  
Qy 1981 CTAGGCGAAGAGGCTTTGGAAAAGTGTCTAGCTGAATGCTATACCTGTCTGAG 2040  
Db 1981 CTAGGCGAAGAGGCTTTGGAAAAGTGTCTAGCTGAATGCTATACCTGTCTGAG 2040  
Qy 2041 CAGGACAAAGATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
Db 2041 CAGGACAAAGATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
Qy 2101 GACTTCAACCGTGAAGGCGAGCTCTGACCAACCTCCAGAGAGAGAGAGAGAGAG 2160  
Db 2101 GACTTCAACCGTGAAGGCGAGCTCTGACCAACCTCCAGAGAGAGAGAGAGAGAG 2160  
Qy 2161 TATGCGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
Db 2161 TATGCGCTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
Qy 2221 GACCTCAACAGATCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
Db 2221 GACCTCAACAGATCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
Qy 2281 CCGGCGACGGAATGAG 2340  
Db 2281 CCGGCGACGGAATGAG 2340  
Qy 2341 ATGCTTACCTGCTGAG 2400  
Db 2341 ATGCTTACCTGCTGAG 2400  
Qy 2401 GTGCGGAG 2460  
Db 2401 GTGCGGAG 2460  
Qy 2461 ACTGACTACTACAG 2520  
Db 2461 ACTGACTACTACAG 2520

Db 2461 ACTGACTACTACAG 2520  
Qy 2521 AGCATCATGATCAGAGAAATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
Db 2521 AGCATCATGATCAGAGAAATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
Qy 2581 TGGAGATTTTCACTATGAGAAACAGGCTGTATACAGCTGTCAACCAATGAGTGA 2640  
Db 2581 TGGAGATTTTCACTATGAGAAACAGGCTGTATACAGCTGTCAACCAATGAGTGA 2640  
Qy 2641 GAGTGTATCACTAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
Db 2641 GAGTGTATCACTAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
Qy 2701 GAGCTGATGCTGGGGGTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
Db 2701 GAGCTGATGCTGGGGGTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
Qy 2761 CATACCTCTCTTCAAGAACTTGGCCAGAGCATCTCGGTCTTACCTGACATTTAGGCTAG 2820  
Db 2761 CATACCTCTCTTCAAGAACTTGGCCAGAGCATCTCGGTCTTACCTGACATTTAGGCTAG 2820  
Qy 2821 GGGCTTTTCCCAAGACGATCTTCCCAAGTACTCTCAAGAGGCTGAGAGAGAGAG 2880  
Db 2821 GGGCTTTTCCCAAGACGATCTTCCCAAGTACTCTCAAGAGGCTGAGAGAGAGAG 2880  
Qy 2881 CATCTTTTAACTGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940  
Db 2881 CATCTTTTAACTGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940  
Qy 2941 ATCAAGAGCTCCGAG 3000  
Db 2941 ATCAAGAGCTCCGAG 3000  
Qy 3001 GTATGACCTTTTGGCATTAATCTCTTCTCTCTTCCATCTCCCTGAGTGTCTT 3060  
Db 3001 GTATGACCTTTTGGCATTAATCTCTTCTCTCTTCCATCTCCCTGAGTGTCTT 3060  
Qy 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
Db 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
Qy 3121 ACCCTTCTTTGATCAATCTGCTTCTGCACTTACTTACTTACTTACTTACTTACTT 3180  
Db 3121 ACCCTTCTTTGATCAATCTGCTTCTGCACTTACTTACTTACTTACTTACTTACTT 3180  
Qy 3181 CTTAACAAGATATTTGTTATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240  
Db 3181 CTTAACAAGATATTTGTTATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240  
Qy 3241 TGCTTGTGTATCTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 3300  
Db 3241 TGCTTGTGTATCTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 3300  
Qy 3301 TAACTTGTGCACTTCTGCTGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Db 3301 TAACTTGTGCACTTCTGCTGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Qy 3361 TTTATTTATTTACTGTTCTTATTTGTTTGGATGAGGCTTAAAGCTGTGTATTTAAAGAA 3420  
Db 3361 TTTATTTATTTACTGTTCTTATTTGTTTGGATGAGGCTTAAAGCTGTGTATTTAAAGAA 3420  
Qy 3421 AACTTGTGTCAATCTGTGAGAGCTTTATCTATGAGAGAGAGAGAGAGAGAGAGAG 3480  
Db 3421 AACTTGTGTCAATCTGTGAGAGCTTTATCTATGAGAGAGAGAGAGAGAGAGAGAG 3480  
Qy 3481 ATTATTTATGAAACCGCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540  
Db 3481 ATTATTTATGAAACCGCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540  
Qy 3541 GTCCCTACTTAAAGAAATCTCAGCACTGTAGCTGAGAGAGAGAGAGAGAGAGAGAG 3600  
Db 3541 GTCCCTACTTAAAGAAATCTCAGCACTGTAGCTGAGAGAGAGAGAGAGAGAGAGAG 3600

QY 3601 CCGAGAGCCTTTCTGAGAGTAAAGACTACTGCGCTCTGTCAGATGATTTCTTT 3660  
DB 3601 CCGAGAGCCTTTCTGAGAGTAAAGACTACTGCGCTCTGTCAGATGATTTCTTT 3660  
QY 3661 TCCCATCAACGAAATGATAGCCGTGAGTGAAGAGCAAAATGGCTT 3707  
DB 3661 TCCCATCAACGAAATGATAGCCGTGAGTGAAGAGCAAAATGGCTT 3707  
RESULT 3  
ABX76427  
ID ABX76427 standard; DNA, 3707 BP.  
AC ABX76427,  
XX  
XX 02-APR-2003 (first entry)  
DT  
XX Lung cancer--associated polynucleotide #291.  
DE  
XX Lung cancer--associated polynucleotide; gene; ds; cytostatic; emphysema;  
KM antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
OS Unidentified.  
XX  
XX MO200286443-A2.  
PN 31-OCT-2002.  
XX  
XX 18-APR-2002; 2002MO-US012476.  
PF  
XX 18-APR-2001; 2001US-0284770P.  
PR 10-MAY-2001; 2001US-0280482P.  
PR 09-NOV-2001; 2001US-0339245P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 29-NOV-2001; 2001US-034370P.  
PR 12-APR-2002; 2002US-0372246P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
PI Aziz N, Murray R;  
XX  
XX WPI; 2003-093161/08.  
DR P-PSDB; ABUS6698.  
DR  
XX  
PT Detecting a lung cancer-associated transcript in a cell from a patient  
PT for treating lung cancer, by contacting a biological sample from the  
PT patient with a polynucleotide that exhibits increased or decreased  
PT expression in lung cancer.  
XX  
PS Claim 22; Page 417; 453pp; English.  
XX  
XX The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridizes  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung cancer-  
CC associated polynucleotides and polypeptides are used for identifying a  
CC compound that modulates a lung cancer-associated polypeptide, for  
CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
CC cancer in a patient and for treating a mammal having lung cancer by  
CC administering a modulatory compound identified. The methods are useful  
CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hypernealastivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antipodles. Sequences  
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the

CC invention  
XX Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 3707; DB 8; Length 3707;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCCATTGCGCATCTAAAGAAATCTGCGCCCCAGAGAGTCCCGAGCGCGCTCGG 60  
DB 1 CCCCATTGCGCATCTAAAGAAATCTGCGCCCCAGAGAGTCCCGAGCGCGCTCGG 60  
QY 61 TCGCCCG 120  
DB 61 TCGCCCG 120  
QY 121 CCCCCTGTAAAGGCGTTGCTGATGCGCGGACACTGTGAACCTTGCGCGCTGCGGAA 180  
DB 121 CCCCCTGTAAAGGCGTTGCTGATGCGCGGACACTGTGAACCTTGCGCGCTGCGGAA 180  
QY 181 CTCTTGCTCGGACCGAGCTCAAGCTCTGTAAAGCTGAGCTGCGACGCGCGCAACG 240  
DB 181 CTCTTGCTCGGACCGAGCTCAAGCTCTGTAAAGCTGAGCTGCGACGCGCGCAACG 240  
QY 241 ACCGAGAGTTAAGAGAGCGCGCAAGCGCGCAAGAGCGCTCCCGCGACGCGTGGG 300  
DB 241 ACCGAGAGTTAAGAGAGCGCGCAAGCGCGCAAGAGCGCTCCCGCGACGCGTGGG 300  
QY 301 CGGCGCGGTGACG 360  
DB 301 CGGCGCGGTGACG 360  
QY 361 TGAATAGGTGAGATGAGACCGCGCATGCGCGCTGCGGCTTCTGCTGCTGCTG 420  
DB 361 TGAATAGGTGAGATGAGACCGCGCATGCGCGCTGCGGCTTCTGCTGCTGCTG 420  
QY 421 GCGCTTGAGAGGCGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 GCGCTTGAGAGGCGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 TGGTGCAGGAGCCCTTCTCGTGCATGCTGAGCAATTCGAGATTGAGCGCTTAA 540  
DB 481 TGGTGCAGGAGCCCTTCTCGTGCATGCTGAGCAATTCGAGATTGAGCGCTTAA 540  
QY 541 GATCCTGAGAAATCAACCGAAATTTTCATGCAAAACGAAAGGTTAGAAATCAT 600  
DB 541 GATCCTGAGAAATCAACCGAAATTTTCATGCAAAACGAAAGGTTAGAAATCAT 600  
QY 601 GAAGATGATTTGAAAGCTTATGCGGACGAGAAATTCGCAATTTGATTTGATTA 660  
DB 601 GAAGATGATTTGAAAGCTTATGCGGACGAGAAATTCGCAATTTGATTTGATTA 660  
QY 661 AAATTTGCTGCTAATAAGATTTCTGAATAACGCAACCTGCGACATCAATTTACC 720  
DB 661 AAATTTGCTGCTAATAAGATTTCTGAATAACGCAACCTGCGACATCAATTTACC 720  
QY 721 CGAAACAACTGAGAGATTTGTCTAGAAACATTTCCGTCACCTTGTCTGAACTG 780  
DB 721 CGAAACAACTGAGAGATTTGTCTAGAAACATTTCCGTCACCTTGTCTGAACTG 780  
QY 781 ATCTGCTGCGGCAATTCATTTACATGCTCTGTGACATTTATGAGATCAAGCTCT 840  
DB 781 ATCTGCTGCGGCAATTCATTTACATGCTCTGTGACATTTATGAGATCAAGCTCT 840  
QY 841 GAGGCTAAATCCAGTCCAGACGCTGAGGATTTGATGCTGATGAAAGAGCAAGAT 900  
DB 841 GAGGCTAAATCCAGTCCAGACGCTGAGGATTTGATGCTGATGAAAGAGCAAGAT 900  
QY 901 ATTCCCTGCGCAACCTGAGATACCAATTTGTTTGGCATCTGCAAAATCTGGCGCA 960  
DB 901 ATTCCCTGCGCAACCTGAGATACCAATTTGTTTGGCATCTGCAAAATCTGGCGCA 960  
QY 961 CTTAACTCACTGTGAGAGAAAGGATTAATCAATTAATCTGATGCTGAGGAGTGAT 1020



Db 961 CCTAACCTGATGAGGAAAGCTATCACTTATCTGTAGTGCAGGTAT 1020  
Qy 1021 CCGGTTCCATATATATATGGAATGTTGGTAACCTGGTTTCCAAACATATGATGAACA 1080  
Db 1021 CCGGTTCCATATATATATGGAATGTTGGTAACCTGGTTTCCAAACATATGATGAACA 1080  
Qy 1081 AGCCACACACAGGCTCTTAAGGATTAATACTTTCATCCGATGACAGTGGAGCAG 1140  
Db 1081 AGCCACACACAGGCTCTTAAGGATTAATACTTTCATCCGATGACAGTGGAGCAG 1140  
Qy 1141 ATCTCTGTGTGGGAAAAATCTGTAGAGAAATCAAGATTCGTCAACTCACTGTG 1200  
Db 1141 ATCTCTGTGTGGGAAAAATCTGTAGAGAAATCAAGATTCGTCAACTCACTGTG 1200  
Qy 1201 CATTTTGACCACTATCACTTCTCGAATCTCCAACTCAGACCACTGGGCACTT 1260  
Db 1201 CATTTTGACCACTATCACTTCTCGAATCTCCAACTCAGACCACTGGGCACTT 1260  
Qy 1261 CCATTCACCTGTGAAGGCAACCCCAACCAAGGCTTCAGTGGTTCTATTAAGGGGCAATA 1320  
Db 1261 CCATTCACCTGTGAAGGCAACCCCAACCAAGGCTTCAGTGGTTCTATTAAGGGGCAATA 1320  
Qy 1321 TTGAATGATCCAAATACATCTGTATCTAATAATACATGTTACCAATCACACGAGTACAC 1380  
Db 1321 TTGAATGATCCAAATACATCTGTATCTAATAATACATGTTACCAATCACACGAGTACAC 1380  
Qy 1381 GCGTCCCTCCAGCTGGATTAATCCCACTGACATGAACATAGGGGACTACCTTAATAGCC 1440  
Db 1381 GCGTCCCTCCAGCTGGATTAATCCCACTGACATGAACATAGGGGACTACCTTAATAGCC 1440  
Qy 1441 AAGATGATAGTGGAGAGATGAGAAACAGATTTCTGCTCACTTCACTGGGCTGGCTGGA 1500  
Db 1441 AAGATGATAGTGGAGAGATGAGAAACAGATTTCTGCTCACTTCACTGGGCTGGCTGGA 1500  
Qy 1501 ATGACGATGTGCAACCCCAATTTATCTGATGTAAATTTATGAAGTTATGAACTGCA 1560  
Db 1501 ATGACGATGTGCAACCCCAATTTATCTGATGTAAATTTATGAAGTTATGAACTGCA 1560  
Qy 1561 GCGAATGACATCGGGGACCAACGAAAGAAATGAATCCCTTCCACGAGCTGCACT 1620  
Db 1561 GCGAATGACATCGGGGACCAACGAAAGAAATGAATCCCTTCCACGAGCTGCACT 1620  
Qy 1621 GATTAACCCGCTCGGGAACATCTCGGCTATGCTGTGATGATGGCTCTGTGCTG 1680  
Db 1621 GATTAACCCGCTCGGGAACATCTCGGCTATGCTGTGATGATGGCTCTGTGCTG 1680  
Qy 1681 GGATTTTGCCTTTGGTAACTGTTTCTGCTTAAAGTTGGCAAGCACTCCAGTTTGGC 1740  
Db 1681 GGATTTTGCCTTTGGTAACTGTTTCTGCTTAAAGTTGGCAAGCACTCCAGTTTGGC 1740  
Qy 1741 ATGAAGGCCCAAGCTCTGCTTATCAGCAATGATGATCTGCGACGCCACTCCATAC 1800  
Db 1741 ATGAAGGCCCAAGCTCTGCTTATCAGCAATGATGATCTGCGACGCCACTCCATAC 1800  
Qy 1801 ATTCCAATGGAGTAACATCTCACTCTTCCGAAAGTGGCCGAGTCTGTCAATT 1860  
Db 1801 ATTCCAATGGAGTAACATCTCACTCTTCCGAAAGTGGCCGAGTCTGTCAATT 1860  
Qy 1861 GGAATGACCAAGATCCCTGTCAATGAAATCCCGAGTCTTGGCATCAACCAAGTCAAG 1920  
Db 1861 GGAATGACCAAGATCCCTGTCAATGAAATCCCGAGTCTTGGCATCAACCAAGTCAAG 1920  
Qy 1921 CTCAAGCCAGACATTTTGTTCAGACATCAAGGCAATTAATCTGCTGCTGCTGAG 1980  
Db 1921 CTCAAGCCAGACATTTTGTTCAGACATCAAGGCAATTAATCTGCTGCTGCTGAG 1980  
Qy 1981 CTAGCGAAGAGCTTTGAAAAGTGTCTAGCTGAATGCTAATACTGCTGCTGAG 2040  
Db 1981 CTAGCGAAGAGCTTTGAAAAGTGTCTAGCTGAATGCTAATACTGCTGCTGAG 2040  
Qy 2041 CAGGACAAAGATCTTGTGTGCAAGTGAAGCCCTGAAGATGCAATGCAAGCAG 2100  
Db 2041 CAGGACAAAGATCTTGTGTGCAAGTGAAGCCCTGAAGATGCAATGCAAGCAG 2100

Db 2041 CAGGACAAAGATCTTGTGTGCAAGTGAAGCCCTGAAGATGCAATGCAAGCAG 2100  
Qy 2101 GACTTCCACCGTGAAGGCGAGCTCTCTGACCAACTCCAGATGAGCACATGCTCAAGTTT 2160  
Db 2101 GACTTCCACCGTGAAGGCGAGCTCTCTGACCAACTCCAGATGAGCACATGCTCAAGTTT 2160  
Qy 2161 TATGGCTCTGCTGAGAGGGGACCCCTCATATGCTCTTTGATGATATGAGATGAG 2220  
Db 2161 TATGGCTCTGCTGAGAGGGGACCCCTCATATGCTCTTTGATGATATGAGATGAG 2220  
Qy 2221 GACCTCAACAGTCTCTCAGGGGACAGGGGCTGATGCGGTGCTGATGAGGAGGCAAC 2280  
Db 2221 GACCTCAACAGTCTCTCAGGGGACAGGGGCTGATGCGGTGCTGATGAGGAGGCAAC 2280  
Qy 2281 CCGCCACCGAATGAGCAGTCCGATGCTGATATAGCCACGAGATGCGCGGCG 2340  
Db 2281 CCGCCACCGAATGAGCAGTCCGATGCTGATATAGCCACGAGATGCGCGGCG 2340  
Qy 2341 ATGGCTTACCTGGGCTCCAGACATTCGTGCAACCGGATTTGGCAACGAACTGCTG 2400  
Db 2341 ATGGCTTACCTGGGCTCCAGACATTCGTGCAACCGGATTTGGCAACGAACTGCTG 2400  
Qy 2401 GTGGGAGAACTTGTCTGTGAATAATGGGGACTTTGGATATGCTCCGGAAGTGTACAGC 2460  
Db 2401 GTGGGAGAACTTGTCTGTGAATAATGGGGACTTTGGATATGCTCCGGAAGTGTACAGC 2460  
Qy 2461 ACTGACTTACAGAGGTCCGTGGGCAACAAATGCTGCACTGCTGGATGCTCCAGAG 2520  
Db 2461 ACTGACTTACAGAGGTCCGTGGGCAACAAATGCTGCACTGCTGGATGCTCCAGAG 2520  
Qy 2521 AGCATCATGTACAGAAATTCACGACGAAAGCGACGCTGGAGCTGGGGGCTGTGTTG 2580  
Db 2521 AGCATCATGTACAGAAATTCACGACGAAAGCGACGCTGGAGCTGGGGGCTGTGTTG 2580  
Qy 2581 TGGGAGATTTTCACTTATGCGAAACAGCCCTGTGTACAGCTGTCAACAAAGAGTGTATA 2640  
Db 2581 TGGGAGATTTTCACTTATGCGAAACAGCCCTGTGTACAGCTGTGTCAACAAAGAGTGTATA 2640  
Qy 2641 GAGGTATACCTGAGGGCCGAGTCTGACAGGACCCCGCAGTCCGACGAGGAGTAT 2700  
Db 2641 GAGGTATACCTGAGGGCCGAGTCTGACAGGACCCCGCAGTCCGACGAGGAGTAT 2700  
Qy 2701 GAGCTGATGCTGGGCTCTGGCAGCAGAGGCCCAATGAGGAAACATCAAGGCGCATC 2760  
Db 2701 GAGCTGATGCTGGGCTCTGGCAGCAGAGGCCCAATGAGGAAACATCAAGGCGCATC 2760  
Qy 2761 CATACCTCTCTTCAAGAACTTGGCCAAAGGCACTCCGGCTTACCTGGAATTTAGGCTAG 2820  
Db 2761 CATACCTCTCTTCAAGAACTTGGCCAAAGGCACTCCGGCTTACCTGGAATTTAGGCTAG 2820  
Qy 2821 GGCCTTTTCCCGACGATCCCTTCCCAAGTATCTCTGAGAGGGGCTGAGAGATGAA 2880  
Db 2821 GGCCTTTTCCCGACGATCCCTTCCCAAGTATCTCTGAGAGGGGCTGAGAGATGAA 2880  
Qy 2881 CATCTTTTAACTGCGCTGAGGCGACCAAGCTCTCTCTTCACTGACAGATTTAAC 2940  
Db 2881 CATCTTTTAACTGCGCTGAGGCGACCAAGCTCTCTCTTCACTGACAGATTTAAC 2940  
Qy 2941 ATCAAGAATCCGAGAACTCTCGAGGGAAGACAGTGTATCTTCTCAATCATAGACACA 3000  
Db 2941 ATCAAGAATCCGAGAACTCTCGAGGGAAGACAGTGTATCTTCTCAATCATAGACACA 3000  
Qy 3001 GTATGACTTCTTTTGGCATATCTCTTCTCTCTTCCATCTGCTTGGTGTCTT 3060  
Db 3001 GTATGACTTCTTTTGGCATATCTCTTCTCTCTTCCATCTGCTTGGTGTCTT 3060  
Qy 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
Db 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
Qy 3121 ACCCTTCTTTTGAATCAATCTGGCTTCTGCAATTAATTAATCTGCAATGACAAAGGC 3180  
Db 3121 ACCCTTCTTTTGAATCAATCTGGCTTCTGCAATTAATTAATCTGCAATGACAAAGGC 3180

QY 3181 CTTAACAAGTAATTTGTTATATACAGACACTCCAGTTTGCCACCACTAACAA 3240  
 DB 3181 CTTAACAAGTAATTTGTTATATACAGACACTCCAGTTTGCCACCACTAACAA 3240  
 QY 3241 TGCCTTGTGATCTCCTGCTTATGATGATGAAAAAGGAAAACAATATTTCAC 3300  
 DB 3241 TGCCTTGTGATCTCCTGCTTATGATGATGAAAAAGGAAAACAATATTTCAC 3300  
 QY 3301 TAAACCTTGCACTTCTGCTGTACAGATTCGAGAGTTTCTATGATTCATTTA 3360  
 DB 3301 TAAACCTTGCACTTCTGCTGTACAGATTCGAGAGTTTCTATGATTCATTTA 3360  
 QY 3361 TTTATTTATTTACTGTTCTTATTTGTTTGGATGCTTAAAGCTGTGTATAAAAAGAA 3420  
 DB 3361 TTTATTTATTTACTGTTCTTATTTGTTTGGATGCTTAAAGCTGTGTATAAAAAGAA 3420  
 QY 3421 AACTGTGTTCAATCTGTGAGAGCTTTATCTATGAGGAAATTAAACGAGAGAAAGAG 3480  
 DB 3421 AACTGTGTTCAATCTGTGAGAGCTTTATCTATGAGGAAATTAAACGAGAGAAAGAG 3480  
 QY 3481 ATTATTTATGAACCGCATATGAGAGAACAAAGAACCACTGGATCACTGTGTCA 3540  
 DB 3481 ATTATTTATGAACCGCATATGAGAGAACAAAGAACCACTGGATCACTGTGTCA 3540  
 QY 3541 GTCCCTTACTTGAAGAAATCTGAGCACTGTTAGCTGGAGAGATGTATTGGCACTTCC 3600  
 DB 3541 GTCCCTTACTTGAAGAAATCTGAGCACTGTTAGCTGGAGAGATGTATTGGCACTTCC 3600  
 QY 3601 CCGTAGAGACCTTTCTGAGAGATTAAGAAAGCACTAGGCTCTGTGTCATGATGATTCCTT 3660  
 DB 3601 CCGTAGAGACCTTTCTGAGAGATTAAGAAAGCACTAGGCTCTGTGTCATGATGATTCCTT 3660  
 QY 3661 TCCCATCAGCAAGAAATGATAGCGTAGAGAGCAAAAGATGCTT 3707  
 DB 3661 TCCCATCAGCAAGAAATGATAGCGTAGAGAGCAAAAGATGCTT 3707

RESULT 4  
 ACF36565  
 ID ACF36565 standard; DNA; 3707 BP.  
 XX  
 AC ACF36565;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human TrkB polypeptide encoding DNA.  
 XX  
 KW TrkB; TrkC; neurodegenerative; neuro-developmental; antiparkinsonian;  
 KW neuroprotective; anticonvulsant; cerebroprotective; vasotrophic;  
 KW neotrophic; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 352..2820  
 FT /\*tag= a  
 FT /product= "TrkB"  
 XX  
 PN MO2003071872-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-MAY-2002; 2002MO-US016807.  
 XX  
 PR 22-FEB-2002; 2002MO-US005151.  
 XX  
 PA (UTMA-) UNIV MARYLAND BALTIMORE.  
 PA (KRUE/) KRUEGER B K.  
 PA (KING/) KINGSBURY T J.  
 PA (BAMB/) BAMBRICK L L.  
 PA (DORS/) DORSEY S G.  
 XX

PI Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;  
 XX WPI, 2003-731549/69.  
 DR P-PSDB; ABR82949.  
 XX  
 DR  
 PT Treating and/or preventing neurodegenerative or neuro-developmental  
 PT disorders, such as Alzheimer's disease, Parkinson's disease and  
 PT amyotrophic lateral sclerosis, using nucleic acids encoding TrkB and/or  
 PT TrkC polypeptides.  
 XX  
 PS Disclosure; Page 56-58; 99pp; English.  
 XX  
 CC The invention relates to treating a neurodegenerative or neuro-  
 CC developmental disorder in a mammal. The method involves altering the  
 CC ratio of the amount of full length TrkB polypeptide to the amount of  
 CC truncated TrkB polypeptides in a neuron or by altering the ratio of the  
 CC amount of full length TrkC polypeptide to the amount of truncated TrkC  
 CC polypeptides in a neuron. The methods and compositions of the present  
 CC invention are useful for treating and/or preventing a neurodegenerative  
 CC or neuro-developmental disorder, such as Alzheimer's disease, Parkinson's  
 CC disease, Huntington's disease, amyotrophic lateral sclerosis (Lou  
 CC Gehrig's disease), the adverse neurologic complications of Down syndrome,  
 CC diabetic peripheral neuropathy and other types of peripheral neuropathy,  
 CC and is associated with an injury to the central or peripheral nervous  
 CC system resulting from stroke, cerebral ischaemia, or chemical and/or  
 CC physical trauma. The present sequence represents a human TrkB polypeptide  
 CC encoding DNA (GenBank Accession No. NM\_006180)  
 XX  
 SQ Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;  
 QY  
 Query Match 100.0%; Score 3707; DB 10; Length 3707;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCATTGCGATCTAAACAAGATCTGCGCCCGAGAGTCCCGAGCGCGGATCGG 60  
 DB 1 CCCCATTGCGATCTAAACAAGATCTGCGCCCGAGAGTCCCGAGCGCGGATCGG 60  
 QY 61 TGCCTGGGCGCGCGGCGATGACGAGCGGCGCGGAGCTTCCAGACGCGATCGC 120  
 DB 61 TGCCTGGGCGCGCGGCGATGACGAGCGGCGCGGAGCTTCCAGACGCGATCGC 120  
 QY 121 CCCCCTGTAAAGGGGTTGCGTATGCGGAGCACTGTGAACCTTGCCTGCGGAAACA 180  
 DB 121 CCCCCTGTAAAGGGGTTGCGTATGCGGAGCACTGTGAACCTTGCCTGCGGAAACA 180  
 QY 121 CCCCCTGTAAAGGGGTTGCGTATGCGGAGCACTGTGAACCTTGCCTGCGGAAACA 180  
 DB 121 CCCCCTGTAAAGGGGTTGCGTATGCGGAGCACTGTGAACCTTGCCTGCGGAAACA 180  
 QY 181 CTCTGCGCTCGGAGCCAGCTCAGGCTGTGATTAAGCTGGAATCGGACAGCCGCAACAGC 240  
 DB 181 CTCTGCGCTCGGAGCCAGCTCAGGCTGTGATTAAGCTGGAATCGGACAGCCGCAACAGC 240  
 QY 241 ACCGAGAGTTTAAGAGAGCCGCAAGCGCAGAGAAAGCTCCCGCAGCGGTGGGGAAAG 300  
 DB 241 ACCGAGAGTTTAAGAGAGCCGCAAGCGCAGAGAAAGCTCCCGCAGCGGTGGGGAAAG 300  
 QY 301 CGGCGGATGCAAGCGCGGAGCAAGGCACTTGGGCTGAGCACTGGCTGATGAGGATGCTCC 360  
 DB 301 CGGCGGATGCAAGCGCGGAGCAAGGCACTTGGGCTGAGCACTGGCTGATGAGGATGCTCC 360  
 QY 361 TGGATTAAGTGGATGGAACCGGCAATGGCGGCTCTGAGGAGCTTGTGCTGAGTGTG 420  
 DB 361 TGGATTAAGTGGATGGAACCGGCAATGGCGGCTCTGAGGAGCTTGTGCTGAGTGTG 420  
 QY 421 GGGCTTGTGAGGGCGGCTTTCGCTGTCCAGTCTGCAATGCAATGCTGCTCGATC 480  
 DB 421 GGGCTTGTGAGGGCGGCTTTCGCTGTCCAGTCTGCAATGCAATGCTGCTCGATC 480  
 QY 481 TGGTGCAGCAACCTTCTCTGCGATGTGGCAATTTCCGAGATTGAGGCTTAACAGTGA 540  
 DB 481 TGGTGCAGCAACCTTCTCTGCGATGTGGCAATTTCCGAGATTGAGGCTTAACAGTGA 540  
 QY 541 GATCTGAGAAACATCAACGAAATTTTCATGCAAAACGAGAAAGTTAGAAATCATCAAC 600  
 DB 541 GATCTGAGAAACATCAACGAAATTTTCATGCAAAACGAGAAAGTTAGAAATCATCAAC 600

OY	601	GAAAGTGAATGTTGAAGCTTATGTGGGACTGAGAAATCTGAACAATTGGATTCTGGATT	660
Db	601	GAAAGTGAATGTTGAAGCTTATGTGGGACTGAGAAATCTGAACAATTGGATTCTGGATT	660
OY	661	AAATTGGGCTCATPAAAGCATTTCTGAAAAACAGAACCTGAGACATPAAATTTTACC	720
Db	661	AAATTGGGCTCATPAAAGCATTTCTGAAAAACAGAACCTGAGACATPAAATTTTACC	720
OY	721	CGAAACAAACGTACGAGTTTGTCTAGAAAACAATTCCTGACCTTGACTGTCTGAAC	780
Db	721	CGAAACAAACGTACGAGTTTGTCTAGAAAACAATTCCTGACCTTGACTGTCTGAAC	780
OY	781	ATCTGTGGGCAATCCATTTCATGTCCTGTGACATTATGTGATCAAGACTCTCCAA	840
Db	781	ATCTGTGGGCAATCCATTTCATGTCCTGTGACATTATGTGATCAAGACTCTCCAA	840
OY	841	GAGGTTAAATCCAGTTCAGACACTCAGGATTTTGTACTGCTGGAATGAAAGCAGAGAAT	900
Db	841	GAGGTTAAATCCAGTTCAGACACTCAGGATTTTGTACTGCTGGAATGAAAGCAGAGAAT	900
OY	901	ATTCCCTGGCAAACTGTGAGATPACCAATTTGGTTGGCATCTGCAATCTGGCCGCA	960
Db	901	ATTCCCTGGCAAACTGTGAGATPACCAATTTGGTTGGCATCTGCAATCTGGCCGCA	960
OY	961	CCTAACCTCACTGTGAGAGAGAAAGTCTATCATTATCTGTAGTGTGCGAGGTAT	1020
Db	961	CCTAACCTCACTGTGAGAGAGAAAGTCTATCATTATCTGTAGTGTGCGAGGTAT	1020
OY	1021	CCGGTTCCTAATATGATATTGGGATGTTGGTAACCTGGTTTCCAAACATATGAATGAACA	1080
Db	1021	CCGGTTCCTAATATGATATTGGGATGTTGGTAACCTGGTTTCCAAACATATGAATGAACA	1080
OY	1081	AGCCACACACAGGGCTCCTTAAGGATPACTTAACATTTCGATCCGATGAGTGGGAAGCAG	1140
Db	1081	AGCCACACACAGGGCTCCTTAAGGATPACTTAACATTTCGATGATGAGTGGGAAGCAG	1140
OY	1141	ATCTCTGTGTGGCGGAAATCTGTGAGAGAGAAGTCAAGATTTCTGCAACCTCACTGTG	1200
Db	1141	ATCTCTGTGTGGCGGAAATCTGTGAGAGAGAAGTCAAGATTTCTGCAACCTCACTGTG	1200
OY	1201	CATTTTGCACCACTATCACATTTCTGAAATCTCAACCTCAGACCACTGTGTCAAT	1260
Db	1201	CATTTTGCACCACTATCACATTTCTGAAATCTCAACCTCAGACCACTGTGTCAAT	1260
OY	1261	CCATTCACTGTGAAAAGGCAACCCCAACAGGCTCACTGTTCTATTAACGGGGCAATA	1320
Db	1261	CCATTCACTGTGAAAAGGCAACCCCAACAGGCTCACTGTTCTATTAACGGGGCAATA	1320
OY	1321	TTGAAATGAGTCCAAATPACATCTGTACTTAAATPACATGTTACCAATCACACGGAGTAC	1380
Db	1321	TTGAAATGAGTCCAAATPACATCTGTACTTAAATPACATGTTACCAATCACACGGAGTAC	1380
OY	1381	GGCTGCTTCAGCTGTGATATCCCACTCAATGAACAATGGGGACTACCTTAATAGCC	1440
Db	1381	GGCTGCTTCAGCTGTGATATCCCACTCAATGAACAATGGGGACTACCTTAATAGCC	1440
OY	1441	AAGAAATGAGTATGAGGAAGATGAGAAACAGATTTCTGCTCACTTCATGGGCTGGCTGGA	1500
Db	1441	AAGAAATGAGTATGAGGAAGATGAGAAACAGATTTCTGCTCACTTCATGGGCTGGCTGGA	1500
OY	1501	ATTGACGATGTGCAAAACCAATTAATCCGATGTAAATTTATGAAGAATTAAGAACGTGCA	1560
Db	1501	ATTGACGATGTGCAAAACCAATTAATCCGATGTAAATTTATGAAGAATTAAGAACGTGCA	1560
OY	1561	GGGAATGACATCGGGGACACAGAACAGAAATGAATGCCATTCCTTCCACAGCGTCACT	1620
Db	1561	GGGAATGACATCGGGGACACAGAACAGAAATGAATGCCATTCCTTCCACAGCGTCACT	1620
OY	1621	GATTAACCCGGTTCGGGAACATCTTCTGGTCTATGCTGTGGTGTGATTTGGCTTGTGGTG	1680
Db	1621	GATTAACCCGGTTCGGGAACATCTTCTGGTCTATGCTGTGGTGTGATTTGGCTTGTGGTG	1680

QY	1661	GGATTTTGGCTTTGGTGAATGCTGTCTTCGTCTTAAGTTGGCAGACACCTCCAAATTGGC	1740
Db	1661	GGATTTTGGCTTTGGTGAATGCTGTCTTCGTCTTAAGTTGGCAGACACCTCCAAATTGGC	1740
QY	1741	ATGAAAGGCCAGCCTCCGTTATCAGGAATGATGATGACTCTGCACGCCACTCCATCAC	1800
Db	1741	ATGAAAGGCCAGCCTCCGTTATCAGGAATGATGATGACTCTGCACGCCACTCCATCAC	1800
QY	1801	ATCTCCATGAGGAGTAAACCTCCATCTTCTTCGGAAAGTGGCCGACAGATGCTGTCAATT	1860
Db	1801	ATCTCCATGAGGAGTAAACCTCCATCTTCTTCGGAAAGTGGCCGACAGATGCTGTCAATT	1860
QY	1861	GGAAATGACCAAGATCCCTGTATTTGAAAATCCCAAGTACTTTGGCATCACCAAGTCAG	1920
Db	1861	GGAAATGACCAAGATCCCTGTATTTGAAAATCCCAAGTACTTTGGCATCACCAAGTCAG	1920
QY	1921	CTCAAGCCAGACATTTGTTTCCAGCATATCAAGGAGATATTAATGTTCTTGAAAAGGGAG	1980
Db	1921	CTCAAGCCAGACATTTGTTTCCAGCATATCAAGGAGATATTAATGTTCTTGAAAAGGGAG	1980
QY	1981	CTAGGCGAAGAGCCTTTGGAAAAGTGTCTAGCTGAATGCTATAACCTCTGTCCAGAG	2040
Db	1981	CTAGGCGAAGAGCCTTTGGAAAAGTGTCTAGCTGAATGCTATAACCTCTGTCCAGAG	2040
QY	2041	CAGACCAAGATCTTGTGTGGCAGTGAAGACCTTGAAAGATGCCAGTGCAATGACCGCAG	2100
Db	2041	CAGACCAAGATCTTGTGTGGCAGTGAAGACCTTGAAAGATGCCAGTGCAATGACCGCAG	2100
QY	2101	GACTTCCACCGTGAAGGCGCAGCTCCCTGACCAACTCCAGATAGAGCAATGTCAATGTC	2160
Db	2101	GACTTCCACCGTGAAGGCGCAGCTCCCTGACCAACTCCAGATAGAGCAATGTCAATGTC	2160
QY	2161	TATGAGCGCTGCGTGAAGGCGACCCCTCATCATGTGCTTTGAGTACATGAAGCATGAGG	2220
Db	2161	TATGAGCGCTGCGTGAAGGCGACCCCTCATCATGTGCTTTGAGTACATGAAGCATGAGG	2220
QY	2221	GACCTCAACAAAGTTCTCAAGGCAACACGCGCCTGAGTCCCTGTGATGAGCTGAAGGCGAC	2280
Db	2221	GACCTCAACAAAGTTCTCAAGGCAACACGCGCCTGAGTCCCTGTGATGAGCTGAAGGCGAC	2280
QY	2281	CCGCCCAAGGAATGGAAGGCACTGAGTCCGCAATGCTGATATAGCCCAAGAGATTCGCCCGCGGC	2340
Db	2281	CCGCCCAAGGAATGGAAGGCACTGAGTCCGCAATGCTGATATAGCCCAAGAGATTCGCCCGCGGC	2340
QY	2341	ATGGCTACACCGGCGTCCACAGCATTTGTGTGACCGGCAATTTGGCCACACAGAACTGCTG	2400
Db	2341	ATGGCTACACCGGCGTCCACAGCATTTGTGTGACCGGCAATTTGGCCACACAGAACTGCTG	2400
QY	2401	GTCGGGGAGAACTTGCTGTGTGAAAAATCGGGGACTTTTGGATGTCCCGGGACGTGTACAGC	2460
Db	2401	GTCGGGGAGAACTTGCTGTGTGAAAAATCGGGGACTTTTGGATGTCCCGGGACGTGTACAGC	2460
QY	2461	ACTGACTATCTACAGGGTTCGTGTGGCCACACAATGCTGCCATTTGCTGTGATGCTTCCAGAG	2520
Db	2461	ACTGACTATCTACAGGGTTCGTGTGGCCACACAATGCTGCCATTTGCTGTGATGCTTCCAGAG	2520
QY	2521	AGCAATCATATGACAGAAATTCACAGACGGAAGGACGCTGTGAGGCTTGGGGGGTGTGTG	2580
Db	2521	AGCAATCATATGACAGAAATTCACAGACGGAAGGACGCTGTGAGGCTTGGGGGGTGTGTG	2580
QY	2581	TGGAGAGATTTTCACTATATGACCAACAGCCTGTGATCCAGCTGTCCAAACAATGAGGTGATA	2640
Db	2581	TGGAGAGATTTTCACTATATGACCAACAGCCTGTGATCCAGCTGTCCAAACAATGAGGTGATA	2640
QY	2641	GAGGTATCACTCAGGGCCGAGTCTTGACAGGACCCCGCACGTGCCCCCAGAGAGTGTAT	2700
Db	2641	GAGGTATCACTCAGGGCCGAGTCTTGACAGGACCCCGCACGTGCCCCCAGAGAGTGTAT	2700
QY	2701	GAGCTGATGCTGGGGGTGTGTGACAGGAGGCCCCCACTGAGGAAGAACTCAAGGGCATC	2760
Db	2701	GAGCTGATGCTGGGGGTGTGTGACAGGAGGCCCCCACTGAGGAAGAACTCAAGGGCATC	2760
QY	2761	CATACCCCTCTTCAGAACTTGCGCCAGGCAATCTCCGCTTACCTGCAATTTCAAGCTAG	2820



Db 61 TGCCTGGGCGCCGGGCGATGCAAGACGCGCGCCGCGAGACTCCGACACCGGTAGCGC 120  
Qy 121 CCCCCTGTAAGCGGATTCCGATGCGGGGACCACTGTGAACCTTGGCGGCTGGCGGAAACA 180  
Db 121 CCCCCTGTAAGCGGATTCCGATGCGGGGACCACTGTGAACCTTGGCGGCTGGCGGAAACA 180  
Qy 181 CTCTTCGCTCCGACCAAGCTAGGCTCTGATTAAGCTGACCTGGGACCGCGGCAACAAGC 240  
Db 181 CTCTTCGCTCCGACCAAGCTAGGCTCTGATTAAGCTGACCTGGGACCGCGGCAACAAGC 240  
Qy 241 ACCGAGAGATTAAAGAGCCGCAAGCGAGGAAAGGCTCCCCGCACGGGTGGGAAAG 300  
Db 241 ACCGAGAGATTAAAGAGCCGCAAGCGAGGAAAGGCTCCCCGCACGGGTGGGAAAG 300  
Qy 301 CGGCGGGGACGCGCGGGGACAGGCACTCGGGCTGGGACCTGGCTGAAGGATGTCGCTCC 360  
Db 301 CGGCGGGGACGCGCGGGGACAGGCACTCGGGCTGGGACCTGGCTGAAGGATGTCGCTCC 360  
Qy 361 TGGATTAAGTGGCAATGACCCGCAATGGCGGGCTCTGGGGCTTCTGGCTGGCTGGTGG 420  
Db 361 TGGATTAAGTGGCAATGACCCGCAATGGCGGGCTCTGGGGCTTCTGGCTGGCTGGTGG 420  
Qy 421 GGGCTTGGAGGGGCGCTTTCGCTGCTCCAGTCTCGCAATGCAAGTGCCTCTCGGATC 480  
Db 421 GGGCTTGGAGGGGCGCTTTCGCTGCTCCAGTCTCGCAATGCAAGTGCCTCTCGGATC 480  
Qy 481 TGGTGGACGACCCCTTCTCCCTGGCAATCGTGGCAATTCGAGAAATGGAGCTTCAAGTGA 540  
Db 481 TGGTGGACGACCCCTTCTCCCTGGCAATCGTGGCAATTCGAGAAATGGAGCTTCAAGTGA 540  
Qy 541 GATCCTGAGAACATCAACGAAATTTTCATCGCAACCGAAGAGTTTGAATGATCAAC 600  
Db 541 GATCCTGAGAACATCAACGAAATTTTCATCGCAACCGAAGAGTTTGAATGATCAAC 600  
Qy 601 GAAGATGATGTTGAAGCTTATGAGGACCTGAGAAATCTGACAAATTTGGATTTGGAATTA 660  
Db 601 GAAGATGATGTTGAAGCTTATGAGGACCTGAGAAATCTGACAAATTTGGATTTGGAATTA 660  
Qy 661 AAATTTTGGGCTCATTAAGCAATTTCTGAAAAACAGCAACCTGACGACATCAATTTTACC 720  
Db 661 AAATTTTGGGCTCATTAAGCAATTTCTGAAAAACAGCAACCTGACGACATCAATTTTACC 720  
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Db 721 CGAAACAACTGACGAGTTTGTCTAGGAAACATTTCCGTGACCTTGAATTTGGAATG 780  
Qy 781 ATCTGCTGGGCAATCCATTTTACATGCTCTGTGACATTAATGAGATCAAGATCTCCAA 840  
Db 781 ATCTGCTGGGCAATCCATTTTACATGCTCTGTGACATTAATGAGATCAAGATCTCCAA 840  
Qy 841 GAGGCTAAATCAAGTCCAGACACTCAGATTTGTATCTGCTGAAATGAAAGCAGCAAGAT 900  
Db 841 GAGGCTAAATCAAGTCCAGACACTCAGATTTGTATCTGCTGAAATGAAAGCAGCAAGAT 900  
Qy 901 ATTCCCTGGGCAACCTGACAGTATCCCAATTTGGTGGTTCGCAATCTGCGGCA 960  
Db 901 ATTCCCTGGGCAACCTGACAGTATCCCAATTTGGTGGTTCGCAATCTGCGGCA 960  
Qy 961 CCTAACTCACTGTGAGGAAAGAAAGTCTATCAATTAATCTGTAGTGGCAGGTGAT 1020  
Db 961 CCTAACTCACTGTGAGGAAAGAAAGTCTATCAATTAATCTGTAGTGGCAGGTGAT 1020  
Qy 1021 CCGGTTCTTAATATGATTTGGAGATGTTGGTAACTGGTTTCCAAACATATGAATGAACA 1080  
Db 1021 CCGGTTCTTAATATGATTTGGAGATGTTGGTAACTGGTTTCCAAACATATGAATGAACA 1080  
Qy 1081 AGGCAACACAGGGGCTCCTTAAGGATATCTAAACATTTCAATCGAGTGAAGTGGGAGAG 1140  
Db 1081 AGGCAACACAGGGGCTCCTTAAGGATATCTAAACATTTCAATCGAGTGAAGTGGGAGAG 1140  
Qy 1141 ATCTCTGTGTGTGGGAAATCTTTGTAGAGAAATCAAGATTTGTCTCAACTGACTGTG 1200  
Db 1141 ATCTCTGTGTGTGGGAAATCTTTGTAGAGAAATCAAGATTTGTCTCAACTGACTGTG 1200

Db 1141 ATCTCTGTGTGTGGGAAATCTTTGTAGAGAAATCAAGATTTGTCTCAACTGACTGTG 1200  
Qy 1201 CATTTTGACCAACTATCACTATTTCTGAAATCTCAACTCTGACACCACTGGTGCAATT 1260  
Db 1201 CATTTTGACCAACTATCACTATTTCTGAAATCTCAACTCTGACACCACTGGTGCAATT 1260  
Qy 1261 CCATTTCACCTGTGAAAGGCAACCCCAACCAAGCGCTTCAAGTGGTTCTATTAACGGGGCAATA 1320  
Db 1261 CCATTTCACCTGTGAAAGGCAACCCCAACCAAGCGCTTCAAGTGGTTCTATTAACGGGGCAATA 1320  
Qy 1321 TTGAAATGATGCCAAATCATCTGTACTTAAATTAATGATTAACCAATCAACGAGATCAAC 1380  
Db 1321 TTGAAATGATGCCAAATCATCTGTACTTAAATTAATGATTAACCAATCAACGAGATCAAC 1380  
Qy 1381 GGGCTGCTCCAGCTGAGTAAATCCCACTCACTGAACATGAGGAGCTACACTCTAATAGCC 1440  
Db 1381 GGGCTGCTCCAGCTGAGTAAATCCCACTCACTGAACATGAGGAGCTACACTCTAATAGCC 1440  
Qy 1441 AAGATGATATGAGGAAAGATGAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTTGA 1500  
Db 1441 AAGATGATATGAGGAAAGATGAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTTGA 1500  
Qy 1501 ATTGACATGCTGCAACCCCAATTTATCTGATGTAATTTTATGAAGATTTAGAACCTGCA 1560  
Db 1501 ATTGACATGCTGCAACCCCAATTTATCTGATGTAATTTTATGAAGATTTATGAACCTGCA 1560  
Qy 1561 GCGAATGACATCGGGGACACACAGACAGAAATGAATGAAATCCCTTCCACAGAGTCACT 1620  
Db 1561 GCGAATGACATCGGGGACACACAGACAGAAATGAATGAAATCCCTTCCACAGAGTCACT 1620  
Qy 1621 GATTAACCCGGTCCGGAAACATCTCTCGGCTATGCTGTGATGATGATGCTGTGGTGG 1680  
Db 1621 GATTAACCCGGTCCGGAAACATCTCTCGGCTATGCTGTGATGATGATGCTGTGGTGG 1680  
Qy 1681 GGAATTTTGCCTTTTGTATATGCTGTTCTGCTTAAGTTGGCAGACACTCCAAATTTGGC 1740  
Db 1681 GGAATTTTGCCTTTTGTATATGCTGTTCTGCTTAAGTTGGCAGACACTCCAAATTTGGC 1740  
Qy 1741 ATGAAAGGCCCAAGCTTCGTTATGAGAAATGAAATGAAATCTGACAGCCCACTCAATAC 1800  
Db 1741 ATGAAAGGCCCAAGCTTCGTTATGAGAAATGAAATGAAATCTGACAGCCCACTCAATAC 1800  
Qy 1801 ATCTCAATGGAATTAACACTCTCTTCCGAAAGTGGCCGAGATGCTGTCAATT 1860  
Db 1801 ATCTCAATGGAATTAACACTCTCTTCCGAAAGTGGCCGAGATGCTGTCAATT 1860  
Qy 1861 GGAATGACCAAGATCCCTGTCAATTTGAATAATCCCAAGTACTTGGCATCAACCAAGTCA 1920  
Db 1861 GGAATGACCAAGATCCCTGTCAATTTGAATAATCCCAAGTACTTGGCATCAACCAAGTCA 1920  
Qy 1921 CTCAAGCAGACACATTTTGTTCAGACATCAAGGACATTAACATTTGTTCTGAAAAAGGAG 1980  
Db 1921 CTCAAGCAGACACATTTTGTTCAGACATCAAGGACATTAACATTTGTTCTGAAAAAGGAG 1980  
Qy 1981 CTAGGCAAGAGGCTTTGAAAAAGTGTCTCTAGCTGAATGCTAATACTCTGTCTGAG 2040  
Db 1981 CTAGGCAAGAGGCTTTGAAAAAGTGTCTCTAGCTGAATGCTAATACTCTGTCTGAG 2040  
Qy 2041 CAGGACAAAGATCTTGTGTGGACATGGAAGACCTGAAAGATGCAAGTGAACATGCAACGCAAG 2100  
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Qy 2101 GACTTTCACCGTGTAGGCGGAGCTCTGACCAACTCCAGCATGAGCACATGTGTCAAGTTC 2160  
Db 2101 GACTTTCACCGTGTAGGCGGAGCTCTGACCAACTCCAGCATGAGCACATGTGTCAAGTTC 2160  
Qy 2161 TATGGGCTGTGGGAGGAGGAGCCCTCATCATGCTTTTGAATGATGATGAAGCATGGG 2220  
Db 2161 TATGGGCTGTGGGAGGAGGAGGAGCCCTCATCATGCTTTTGAATGATGATGAAGCATGGG 2220  
Qy 2221 GACCTCAACAGTTTCTCAAGGACACAGGCGCTGTAGTCCGTGTGATGCTGAGGCAAC 2280  
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QY 2281 CCGGCCACGGAACTGAGCGAGTGGCAGATGCTGCATATAGCCCAAGCATGCGCCGGGC 2340  
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 QY 2241 ATGGCTACCGTGGGCGCCAGACATTCGTGACCGGCATTTGGGACACAGGAACTGGCTG 2400  
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 DB 2401 GTCGGGAGAACTTGTGTGTGAAAATCGGGGACTTTGGGATGTCCGGGACGTGTACAGC 2460  
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 DB 2461 ACTGACTACTACAGGGTGTGTGCGCACATGCTGCCATTTGGCTGATGCTTCAGAG 2520  
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 DB 2521 AGCATCATGTACAGGAAATTCAGACGGAAAGCGACTGGGAGCTGGGGGTGTGTG 2580  
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 DB 2581 TGGGAGATTTTCACTATGCGAAACAGCCCTGTATCCAGCTGTGCAAACAATGAGGTATA 2640  
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 DB 3001 GTATTGACTTCTTTTGGCATTAATCTCTTCTCTCTTTCATCTCCCTGGTGTCTCT 3060  
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 DB 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
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 DB 3121 ACCCTTCTTTTGAATCATCTGCTTCTGCAATTAATTAATCTGATAGCAAAAGGC 3180  
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 DB 3181 CTTTAAACAAAGTAAATTTGTATATCAGAGACATCTCCAGTTTGGCCACACAACATAACA 3240  
 QY 3241 TGCCTTGTGTATCTGCTCTTTGATGTGATGTAAGAAAAAGGAAAAAGAAATATTTCACT 3300  
 DB 3241 TGCCTTGTGTATCTGCTCTTTGATGTGATGTAAGAAAAAGGAAAAAGAAATATTTCACT 3300  
 QY 3301 TAAACTTTGTCACTTCTGCTGTACAGATATGAGAGTTTCTATGATTCATCTTATTTA 3360  
 DB 3301 TAAACTTTGTCACTTCTGCTGTACAGATATGAGAGTTTCTATGATTCATCTTATTTA 3360

QY 3361 TTTATATTATTACTGTTCTTATTTGTTTTGATGCTTAAGCTGTGTAATAAAAAAGAA 3420  
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 DB 3421 AACTTGTTCATCTGTGAAGCTTTATCTATGAGAGATTTAAACACAGAGAAAGAG 3480  
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 DB 3661 TCCCATCACCAAAATGATAGCGTGCAGTAGAGAGCAAAAGATGCTT 3707  
 RESULT 6  
 ADN39075  
 ID ADN39075 standard; cDNA; 3707 BP.  
 XX  
 AC ADN39075;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:393.  
 XX  
 KW Human, differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; lechemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularization syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
 KW vulnetary; gene therapy; vaccine; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN W02003042661-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 13-NOV-2002; 2002WC-US036810.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334393P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368809P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 05-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397757P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (BOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;



PI Mack DH, Murray R, Watson SR, Wilson KE, Ziolknik A;  
XX WPI: 2003-468649/44.  
DR P-PSDB; ADN39076.  
XX  
PT Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX  
PS Claim 8; SEQ ID NO 393; 1385bp; English.  
XX  
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; use of such antibodies for drug targeting;  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neurovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a nucleic acid sequence of the invention.  
XX  
SQ Sequence 3707 BP; 942 A; 948 C; 900 G; 917 T; 0 U; 0 Other;  
Query Match 100.0%; Score 3707; DB 11; Length 3707;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCCCATTCGATCTTAACAGAGATCTGCGCCGAGAGATCCCGAGCGCCGCGTGG 60  
DB 1 CCCCCATTCGATCTTAACAGAGATCTGCGCCGAGAGATCCCGAGCGCCGCGTGG 60  
QY 61 TCCCCCGGCGCCCGGCGCATGAGAGAGCGCGCGCGGAGCTCCGAGACGGGTAGCGC 120  
DB 61 TCCCCCGGCGCCCGGCGCATGAGAGAGCGCGCGCGGAGCTCCGAGACGGGTAGCGC 120  
QY 121 CCCCCGTTAAAGCGGTTGCTATGCGCGGAGCACTGTGAACTCGCGCGCTGCGGGAACA 180  
DB 121 CCCCCGTTAAAGCGGTTGCTATGCGCGGAGCACTGTGAACTCGCGCGCTGCGGGAACA 180  
QY 181 CTCTTCGCTCCGAGACAGACTGAGCTCTGTATAGCTGTGACTCGGACCGCGCAACAGC 240  
DB 181 CTCTTCGCTCCGAGACAGACTGAGCTCTGTATAGCTGTGACTCGGACCGCGCAACAGC 240  
QY 241 ACCGAGAGTTAAGAGAGCCCGAGAGCGAGAGCGCTCCCGCGACGGGTGGGGGAAAG 300  
DB 241 ACCGAGAGTTAAGAGAGCCCGAGAGCGAGAGCGCTCCCGCGACGGGTGGGGGAAAG 300  
QY 301 CGGCGGAGGAGCGGAGGAGAGAGCACTCGGCGTGGCACTGGGCTGAGTGGGATGTC 360  
DB 301 CGGCGGAGGAGCGGAGGAGAGAGCACTCGGCGTGGCACTGGGCTGAGTGGGATGTC 360  
QY 361 TGGATTAAGTGGAGTGAACCCGCGCATGCGCGCTCTGCGGCTTCTGCTGCTGCTG 420  
DB 361 TGGATTAAGTGGAGTGAACCCGCGCATGCGCGCTCTGCGGCTTCTGCTGCTGCTG 420  
QY 421 GCGCTTCTGAGAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 421 GCGCTTCTGAGAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 TGGTGAAGAGAGCCCTTCTCTGAGCATGAGTGGATTTGAGATTGGAGCTTAAGAGTGA 540  
DB 481 TGGTGAAGAGAGCCCTTCTCTGAGCATGAGTGGATTTGAGATTGGAGCTTAAGAGTGA 540  
QY 541 GATCTGAGAACATCAGGAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAAC 600  
DB 541 GATCTGAGAACATCAGGAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAAC 600

DB 541 GATCTGAGAACATCAGGAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAAC 600  
QY 601 GAAGATGATGTTGAAGCTTATGTTGGAGCTGAGAAATCTGACATATTGGATTGCAATTA 660  
DB 601 GAAGATGATGTTGAAGCTTATGTTGGAGCTGAGAAATCTGACATATTGGATTGCAATTA 660  
QY 661 AAATTTGTGCTCAVAAAGCATTTTCTGAAAAAGCAACCTGACAGACATCAATTTTACC 720  
DB 661 AAATTTGTGCTCAVAAAGCATTTTCTGAAAAAGCAACCTGACAGACATCAATTTTACC 720  
QY 721 CGAAACCAATGACAGAGTTTGTCTAGGAAACATTTCCGTACCTTGAATGCTGAACTG 780  
DB 721 CGAAACCAATGACAGAGTTTGTCTAGGAAACATTTCCGTACCTTGAATGCTGAACTG 780  
QY 781 ATTCGAGGCGCAATTCATTAACAGCTCCGTGACATTAATGAGTATGAGATCTTCCAA 840  
DB 781 ATTCGAGGCGCAATTCATTAACAGCTCCGTGACATTAATGAGTATGAGATCTTCCAA 840  
QY 841 GAGGCTAAATCCAGTCCAGACACTCAGGATTTGTACTGCTGAAATGAAAGCAGAGAT 900  
DB 841 GAGGCTAAATCCAGTCCAGACACTCAGGATTTGTACTGCTGAAATGAAAGCAGAGAT 900  
QY 901 ATTCCCTGGCAAACTGCGAGATACCAATTTGCTTCCATCTGCAATCTGCGCGCA 960  
DB 901 ATTCCCTGGCAAACTGCGAGATACCAATTTGCTTCCATCTGCAATCTGCGCGCA 960  
QY 961 CCTAACCTACTGTGAGAGAGAGAGATCTATCACTTATCTGTAGTGGAGGTAT 1020  
DB 961 CCTAACCTACTGTGAGAGAGAGAGATCTATCACTTATCTGTAGTGGAGGTAT 1020  
QY 1021 CCGGTTCTTAATATGATTTGGATGTTGTAACTCGTTTCAAAACATATGATGAACA 1080  
DB 1021 CCGGTTCTTAATATGATTTGGATGTTGTAACTCGTTTCAAAACATATGATGAACA 1080  
QY 1081 AGCCACACAGGCGCTCTTAAGATTACTAACATTTTCATGCAATGACAGTGGAGAG 1140  
DB 1081 AGCCACACAGGCGCTCTTAAGATTACTAACATTTTCATGCAATGACAGTGGAGAG 1140  
QY 1141 ATCTCTGTGTGGGAGAAATCTGTGTGAGAGATGAAATGCTGTCACTGCTG 1200  
DB 1141 ATCTCTGTGTGGGAGAAATCTGTGTGAGAGATGAAATGCTGTCACTGCTG 1200  
QY 1201 CATTTTGCACCACTATCACTATTTCTGCAATCTGCAACCTGACAGCACCTGCTGAT 1260  
DB 1201 CATTTTGCACCACTATCACTATTTCTGCAATCTGCAACCTGACAGCACCTGCTGAT 1260  
QY 1261 CCATTTCACTGTAAGAGCAACCCCAACCAAGCGCTTCACTGATGTTCTATTAAGGGGCAATTA 1320  
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DB 1321 TTGAATGATGCAATTAATCTGTATCTTAATAATTAATTAATTAATTAATTAATTAATTA 1380  
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DB 1381 GCGTCCCTCCAGCTGAGTAACTCCACTCACTGAACAAATGAGGAGCTACACTTAATAGC 1440  
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DB 1441 AAGATGATGTAAGAGAGATGAGAAACAGATTTCTGCTCACTTATGAGGCTGCTGGA 1500  
QY 1501 ATTGACGATGATGCAAAACCCAAATTAATCTGATGTAATTAATTAATTAATTAATTAATTA 1560  
DB 1501 ATTGACGATGATGCAAAACCCAAATTAATCTGATGTAATTAATTAATTAATTAATTAATTA 1560  
QY 1561 GCGAATGACATCGGAGGACCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1620  
DB 1561 GCGAATGACATCGGAGGACCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1620  
QY 1621 GATTAACACCGGTCGGGAAACATCTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
DB 1621 GATTAACACCGGTCGGGAAACATCTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1680

1  
QY 1681 GGATTTTGGCTTTTGGTAATGCTGTCTGCTTAAGTTGGCAAGACACTCCAAATTGGC 1740  
Db 1681 GGATTTTGGCTTTTGGTAATGCTGTCTGCTTAAGTTGGCAAGACACTCCAAATTGGC 1740  
QY 1741 ATGAAAGGCCAGGCTCGGTATACAGAAATGATGATGCTGCGAGCCCACTGCATCAC 1800  
Db 1741 ATGAAAGGCCAGGCTCGGTATACAGAAATGATGATGCTGCGAGCCCACTGCATCAC 1800  
QY 1801 ATCTCAATGGAGTAACAATCTCATCTTCTTGGAGGTGGCCGAGATGCTGATTAAT 1860  
Db 1801 ATCTCAATGGAGTAACAATCTCATCTTCTTGGAGGTGGCCGAGATGCTGATTAAT 1860  
QY 1861 GGAATGACCAAGATCCCTGTCTATTTGAAAATGCCCAATGATTTGGCATCACCAAGTCAG 1920  
Db 1861 GGAATGACCAAGATCCCTGTCTATTTGAAAATGCCCAATGATTTGGCATCACCAAGTCAG 1920  
QY 1921 CTCAAGCGACAGACATTTGTTGACGACATCAAGCGACATTAATTTGTTCTGAAAAGGAG 1980  
Db 1921 CTCAAGCGACAGACATTTGTTGACGACATCAAGCGACATTAATTTGTTCTGAAAAGGAG 1980  
QY 1981 CTAGCGAAGAGAGCTTTGAAAAGTGTCTCTAGCTGAATGCTAATACCTGTCTGAG 2040  
Db 1981 CTAGCGAAGAGAGCTTTGAAAAGTGTCTCTAGCTGAATGCTAATACCTGTCTGAG 2040  
QY 2041 CAGGACAAAGATCTTGTGTGACGTAAGACCTTGAAAGATGCCAATGACATGACGCAAG 2100  
Db 2041 CAGGACAAAGATCTTGTGTGACGTAAGACCTTGAAAGATGCCAATGACATGACGCAAG 2100  
QY 2101 GACTTCCACCGTGAAGGCGAGACTCTGACCAACCTCCAGCATGAGCATGTCAAGTTC 2160  
Db 2101 GACTTCCACCGTGAAGGCGAGACTCTGACCAACCTCCAGCATGAGCATGTCAAGTTC 2160  
QY 2161 TATGCGCTGTGCGTGAAGGCGAACCCCTCATCATGTCTTTGATGATGATGATGATGATG 2220  
Db 2161 TATGCGCTGTGCGTGAAGGCGAACCCCTCATCATGTCTTTGATGATGATGATGATGATG 2220  
QY 2221 GACCTCAACAAGTTCCTCAAGGCGACAGGCGCTGATGCTGCTGATGATGATGATGATG 2280  
Db 2221 GACCTCAACAAGTTCCTCAAGGCGACAGGCGCTGATGCTGCTGATGATGATGATGATG 2280  
QY 2281 CCGCGCACGGAATCTGACGAGTGCAGATGCTGATATAGCCAGAGATGCGCGGCG 2340  
Db 2281 CCGCGCACGGAATCTGACGAGTGCAGATGCTGATATAGCCAGAGATGCGCGGCG 2340  
QY 2341 ATGCTTACCTGTGCGTCCAGACATTCGTGACCCGCAATTTGGCACCAAGAACTGCTG 2400  
Db 2341 ATGCTTACCTGTGCGTCCAGACATTCGTGACCCGCAATTTGGCACCAAGAACTGCTG 2400  
QY 2401 GTGCGGAGAACTTGTGTGAAAATCGGGGACTTTGGGATGTCCCGGAGCTGTACAGC 2460  
Db 2401 GTGCGGAGAACTTGTGTGAAAATCGGGGACTTTGGGATGTCCCGGAGCTGTACAGC 2460  
QY 2461 ACTGACTACTACAGAGTGTGCGACACAAATGCTGCCATTCGCTGGAATGCCCTCAAG 2520  
Db 2461 ACTGACTACTACAGAGTGTGCGACACAAATGCTGCCATTCGCTGGAATGCCCTCAAG 2520  
QY 2521 AGCATCATGTACAGAAATTTCAAGACGGAAGCGACGCTGTGAGACCTGGGGGTGTGTG 2580  
Db 2521 AGCATCATGTACAGAAATTTCAAGACGGAAGCGACGCTGTGAGACCTGGGGGTGTGTG 2580  
QY 2581 TGGAGATTTTCACTTATGCAAAACAGCCTGTGTACAGCTGTCAAAATGAGGTGATA 2640  
Db 2581 TGGAGATTTTCACTTATGCAAAACAGCCTGTGTACAGCTGTGTCAAAATGAGGTGATA 2640  
QY 2641 GAGGTATCACTCAAGGCGGAGTCTGTGAGAGACCCCGCAAGTCCCGCCAGAGATGTAT 2700  
Db 2641 GAGGTATCACTCAAGGCGGAGTCTGTGAGAGACCCCGCAAGTCCCGCCAGAGATGTAT 2700  
QY 2701 GAGCTGATGTCTGGGTGTGCGACGAGAGCCCGCATGAGAAAGAACTAAGGCGATC 2760  
Db 2701 GAGCTGATGTCTGGGTGTGCGACGAGAGCCCGCATGAGAAAGAACTAAGGCGATC 2760

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QY 2821 GGCCTTTTCCGAGACCGATTCCTTCCCAAGTACTCTGACAGCGGCTGAGAGATGAA 2880  
Db 2821 GGCCTTTTCCGAGACCGATTCCTTCCCAAGTACTCTGACAGCGGCTGAGAGATGAA 2880  
QY 2881 CATCTTTTAACTGCGCTGAGAGGCGACCAAGCTGTCTCTTCACTGTGACATTAAT 2940  
Db 2881 CATCTTTTAACTGCGCTGAGAGGCGACCAAGCTGTCTCTTCACTGTGACATTAAT 2940  
QY 2941 ATCAAGACTCCGAGAAAGCTCTGAGGGAAGAGTGTACTTCTTCACTATAGACACA 3000  
Db 2941 ATCAAGACTCCGAGAAAGCTCTGAGGGAAGAGTGTACTTCTTCACTATAGACACA 3000  
QY 3001 GATATGACTCTTTTGGCATTAATCTCTTCTCTCTTCCATGCTCCCTGTGTTCTT 3060  
Db 3001 GATATGACTCTTTTGGCATTAATCTCTTCTCTCTTCCATGCTCCCTGTGTTCTT 3060  
QY 3061 TTTCTTTTAAATTTCTTTTCTTTCTTTTCTTTTCTTCCCTGCTTCAAGATCTT 3120  
Db 3061 TTTCTTTTAAATTTCTTTTCTTTCTTTTCTTTTCTTCCCTGCTTCAAGATCTT 3120  
QY 3121 ACCCTTCTTTTGAATCAATCTGCTTGCATTAATTAATTAATGATGATGATGATGATG 3180  
Db 3121 ACCCTTCTTTTGAATCAATCTGCTTGCATTAATTAATTAATGATGATGATGATGATG 3180  
QY 3181 CTTAACAAAGTAATTTGATATACAGACAGACACTCCAGTTTCCCAACCACTAACA 3240  
Db 3181 CTTAACAAAGTAATTTGATATACAGACAGACACTCCAGTTTCCCAACCACTAACA 3240  
QY 3241 TGCCTGTGTATCTGCTCTTGTATGTGATGATGATGATGATGATGATGATGATGATG 3300  
Db 3241 TGCCTGTGTATCTGCTCTTGTATGTGATGATGATGATGATGATGATGATGATGATG 3300  
QY 3301 TAAACTTGTCACTTGTGCTGTAACAGATATGAGAGATTTATGATGATGATGATGATG 3360  
Db 3301 TAAACTTGTCACTTGTGCTGTAACAGATATGAGAGATTTATGATGATGATGATGATG 3360  
QY 3361 TTTATTTATTTACTGTTCTTATTTGTTTGAATGCTTAAGCTGTGTATTAATAAGAA 3420  
Db 3361 TTTATTTATTTACTGTTCTTATTTGTTTGAATGCTTAAGCTGTGTATTAATAAGAA 3420  
QY 3421 AACTTGTTCATCTGTGAAAGCTTTATCTATGAGAGATTAATAACAGAGAAAGAG 3480  
Db 3421 AACTTGTTCATCTGTGAAAGCTTTATCTATGAGAGATTAATAACAGAGAAAGAG 3480  
QY 3481 ATTTATTTATGAACCGCAATATGAGAGAAACAACAACAGTGGATTCAGCTGTGTCA 3540  
Db 3481 ATTTATTTATGAACCGCAATATGAGAGAAACAACAACAGTGGATTCAGCTGTGTCA 3540  
QY 3541 GTCCCTACTTAGGAAATACACAGACTGTAGCTGGAGAAATGTATTTGGGCACTTCC 3600  
Db 3541 GTCCCTACTTAGGAAATACACAGACTGTAGCTGGAGAAATGTATTTGGGCACTTCC 3600  
QY 3601 CTTGAGACCTTTCTGAGAGTAAAGAAAGCTAAGCTGTGTGCTGTGATGATGATGATG 3660  
Db 3601 CTTGAGACCTTTCTGAGAGTAAAGAAAGCTAAGCTGTGTGCTGTGATGATGATGATG 3660  
QY 3661 TCCCATACCAAGAAATGATAGCGTGCAGTGAAGCAAAAGATGCTT 3707  
Db 3661 TCCCATACCAAGAAATGATAGCGTGCAGTGAAGCAAAAGATGCTT 3707

RESULT: 7  
ADN39737 standard; cDNA; 3707 BP.  
XX ADN39737;  
XX AC  
XX XX  
DT 17-JUN-2004 (first entry)  
XX

DB Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C109;  
 XX Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularization syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
 KW vulnery; gene therapy; vaccine; gene; ss.  
 XX Homo sapiens.  
 XX WO2003042661-A2.  
 PD 22-MAY-2003.  
 XX 13-NOV-2002; 2002WO-US036810.  
 PF 13-NOV-2002; 2002US-0350666P.  
 XX 13-NOV-2001; 2001US-0332464P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0332464P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368099P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 05-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX (EBSB-) EOS BIOTECHNOLOGY INC.  
 PA Afar D, Aziz N, Ginsburg WM, Gish KC, Glyme R, Hevezi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
 XX WPI; 2003-468649/44.  
 DR P-PSDB; ADN39954.  
 XX Determining the presence or absence of a pathological cell in a patient,  
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
 PT a nucleic acid in a biological sample.  
 XX  
 XX Claim 8; SEQ ID NO C109; 1385bp; English.  
 PS The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angiotensin or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularization syndromes, scarring, and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a nucleic acid sequence of the invention.  
 XX  
 SQ Sequence 3707 BP, 942 A, 948 C, 900 G, 917 T, 0 U, 0 Other;

	Matches 3707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1	CCCCATTTCGATCTAACAAGAAATCGCCGCCAGAGATCCCGACGCGCGCGTGG 60
DB 1	CCCCATTTCGATCTAACAAGAAATCGCCGCCAGAGATCCCGACGCGCGCGTGG 60
QY 61	TGCCCG 120
DB 61	TGCCCG 120
QY 121	CCCCCTGTAAGCGGCTTCGTAATGCGCGGACCACTGTGAAACCTCCGCGCGCGGAA 180
DB 121	CCCCCTGTAAGCGGCTTCGTAATGCGCGGACCACTGTGAAACCTCCGCGCGGAA 180
QY 181	CTCTTCGCTCCGACGACGCTCAGCCTCTGATTAAGCTGAGTCTCGGACGCGCGGAAAG 240
DB 181	CTCTTCGCTCCGACGACGCTCAGCCTCTGATTAAGCTGAGTCTCGGACGCGCGGAAAG 240
QY 241	ACCGAGAGATTAAAGAGACCGCAAGCGCAAGGAAAGGCTCCCGCACGCGGTGGGAAAG 300
DB 241	ACCGAGAGATTAAAGAGACCGCAAGCGCAAGGAAAGGCTCCCGCACGCGGTGGGAAAG 300
QY 301	CGGCGCGGTGACG 360
DB 301	CGGCGCGGTGACG 360
QY 361	TGATTAAGTGGGCACTGGAACCGCGCATGGCGCGCTGCGGCGCTTCTGCTGGCTGGT 420
DB 361	TGATTAAGTGGGCACTGGAACCGCGCATGGCGCGCTGCGGCGCTTCTGCTGGCTGGT 420
QY 421	GGCTTCGAGAGGCGCGCTTCGCTGCTCCGACGTCGTAATGCAATGCTGCTCGATC 480
DB 421	GGCTTCGAGAGGCGCGCTTCGCTGCTCCGACGTCGTAATGCAATGCTGCTCGATC 480
QY 481	TGGTGACGCGACCTTCTCTCTGCGCATGCTGCGCATTTCCGAGATTGAGCTTAACAGTGA 540
DB 481	TGGTGACGCGACCTTCTCTCTGCGCATGCTGCGCATTTCCGAGATTGAGCTTAACAGTGA 540
QY 541	GATCCTGAGAACATCAGCAAAATTTTCATGCGCAACGAAAGAGTTAGAAATCATCAAC 600
DB 541	GATCCTGAGAACATCAGCAAAATTTTCATGCGCAACGAAAGAGTTAGAAATCATCAAC 600
QY 601	GAAATGATGTTGAAGCTTAATGTTGAGGACTGAGAAATCTGCAATTTGATTTGATTA 660
DB 601	GAAATGATGTTGAAGCTTAATGTTGAGGACTGAGAAATCTGCAATTTGATTTGATTA 660
QY 661	AAATTTGCTCATTAAGCAATTTCTGAAACAGCAACCTGACGACATCAATTTTAAAC 720
DB 661	AAATTTGCTCATTAAGCAATTTCTGAAACAGCAACCTGACGACATCAATTTTAAAC 720
QY 721	CGAAACAACTGACGAGTTTGTCTAGGAAACATTTCCGTACCTTGACTGTCTGAAC 780
DB 721	CGAAACAACTGACGAGTTTGTCTAGGAAACATTTCCGTACCTTGACTGTCTGAAC 780
QY 781	ATTCGTGAGGCAATCAATTTAATGCTCTGTTGACATTTATGTTGATTAAGACTCTCAA 840
DB 781	ATTCGTGAGGCAATCAATTTAATGCTCTGTTGACATTTATGTTGATTAAGACTCTCAA 840
QY 841	GAGGCTAAATTCAGTCCAGACACTCAGAGATTGATGCTGTAATGAAGCAGCAAGAT 900
DB 841	GAGGCTAAATTCAGTCCAGACACTCAGAGATTGATGCTGTAATGAAGCAGCAAGAT 900
QY 901	ATTCCTGCGCAACCTGCGGATTCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901	ATTCCTGCGCAACCTGCGGATTCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961	CTTAACCTCACTGAGGAGAAAGTATACATTAATCTGATGCTGAGTATGCTGAGTAT 1020
DB 961	CTTAACCTCACTGAGGAGAAAGTATACATTAATCTGATGCTGAGTATGCTGAGTAT 1020
QY 1021	CCGCTTCCTAATATGATTTGAGATGTTGTTAAGCTGCTTTCGAAATATGATGAAGAA 1080
DB 1021	CCGCTTCCTAATATGATTTGAGATGTTGTTAAGCTGCTTTCGAAATATGATGAAGAA 1080

Query Match 100.0%; Score 3707; DB 11; Length 3707;  
 Best Local Similarity 100.0%; Pred. No. 0;

QY 1081 AGCCACACAGGSGCTCCTTAAGATACTAACATTTTCATCCGATGACAGTGGAGAG 1140  
DB 1081 AGCCACACAGGSGCTCCTTAAGATACTAACATTTTCATCCGATGACAGTGGAGAG 1140  
QY 1141 ATCTCTGTGTGGGAAAATCTTGTAGAGAGATGAAGATCTGTCAACTCACTGTG 1200  
DB 1141 ATCTCTGTGTGGGAAAATCTTGTAGAGAGATGAAGATCTGTCAACTCACTGTG 1200  
QY 1201 CATTTGACCAACATATCACTTTCTCGAATCTCCAACCTCAGACCACTGGTGAT 1260  
DB 1201 CATTTGACCAACATATCACTTTCTCGAATCTCCAACCTCAGACCACTGGTGAT 1260  
QY 1261 CCATTCACTGTGAAGGCAACCCCAACCAAGCGCTTCAAGTGTCTATAACGGGGCA 1320  
DB 1261 CCATTCACTGTGAAGGCAACCCCAACCAAGCGCTTCAAGTGTCTATAACGGGGCA 1320  
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QY 1381 GGCTGCTCCAGCTGATTAATCCCACTCACATGAACAATGGGAGCTACACTTAATGCC 1440  
DB 1381 GGCTGCTCCAGCTGATTAATCCCACTCACATGAACAATGGGAGCTACACTTAATGCC 1440  
QY 1441 AAGATATGATGTGGGAAGATGAGAAAACAGATTTCTGCTCATTCAAGGCTGAC 1500  
DB 1441 AAGATATGATGTGGGAAGATGAGAAAACAGATTTCTGCTCATTCAAGGCTGAC 1500  
QY 1501 ATTGACATGTGTGAACCCCAATTAATCCGATGTAATTAATGAAGTTATGGAAC 1560  
DB 1501 ATTGACATGTGTGAACCCCAATTAATCCGATGTAATTAATGAAGTTATGGAAC 1560  
QY 1561 GCGAATGACATCGGGGACACCAACGAAGAATGAATAATCCCTTCCACAGAGTCACT 1620  
DB 1561 GCGAATGACATCGGGGACACCAACGAAGAATGAATAATCCCTTCCACAGAGTCACT 1620  
QY 1621 GATTAACCCGCTCGGGAACATCTCTCGGCTAATCTGTGTGTGTGTGTGTGTGT 1680  
DB 1621 GATTAACCCGCTCGGGAACATCTCTCGGCTAATCTGTGTGTGTGTGTGTGTGT 1680  
QY 1681 GGATTTTGGCTTTGTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
DB 1681 GGATTTTGGCTTTGTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
QY 1741 ATGAAGGCGCCAGCTCGGTTATCAGCAATGATGATCTGTGCAAGCCCATCTCATAC 1800  
DB 1741 ATGAAGGCGCCAGCTCGGTTATCAGCAATGATGATCTGTGCAAGCCCATCTCATAC 1800  
QY 1801 ATCTCAATGGAGTAACTCATCTTTCTGGAAGGTGGCCAGATGCTGTATATT 1860  
DB 1801 ATCTCAATGGAGTAACTCATCTTTCTGGAAGGTGGCCAGATGCTGTATATT 1860  
QY 1861 GGAATGACCAAGATCCCTGTATATGAAAATGCCAGATCTTTGGCATCAACAAAGTAC 1920  
DB 1861 GGAATGACCAAGATCCCTGTATATGAAAATGCCAGATCTTTGGCATCAACAAAGTAC 1920  
QY 1921 CTCAAGCAGACATTTGTTCAGCACTCAAGGACATTAACATTTGTTCTGAAAAGGAG 1980  
DB 1921 CTCAAGCAGACATTTGTTCAGCACTCAAGGACATTAACATTTGTTCTGAAAAGGAG 1980  
QY 1981 CTAGGCGAAGAGCCTTTGAAAAGTGTCTAGCTGAATCTATAACCTGTCTGTAG 2040  
DB 1981 CTAGGCGAAGAGCCTTTGAAAAGTGTCTAGCTGAATCTATAACCTGTCTGTAG 2040  
QY 2041 CAGACAAAGATCTTGTGTGTGTGAAGCCTTGAAGATGCGATGACAAATGACGCAAG 2100  
DB 2041 CAGACAAAGATCTTGTGTGTGTGAAGCCTTGAAGATGCGATGACAAATGACGCAAG 2100  
QY 2101 GACTTCCACGCTGAGGCGAGACTCTGACCAACCTCCAGATGAGCACTGTCAAGTTC 2160  
DB 2101 GACTTCCACGCTGAGGCGAGACTCTGACCAACCTCCAGATGAGCACTGTCAAGTTC 2160

QY 2161 TATGGGCTGTGGTGGAGGGGCAACCCCTCATATAGTCTTTTAAATACATGAAGCATGG 2220  
DB 2161 TATGGGCTGTGGTGGAGGGGCAACCCCTCATATAGTCTTTTAAATACATGAAGCATGG 2220  
QY 2221 GACCTCAACAAATGCTCTCAGGGGACACAGGCGCTGATAGCGGTGTGTGTGTGTGTGT 2280  
DB 2221 GACCTCAACAAATGCTCTCAGGGGACACAGGCGCTGATAGCGGTGTGTGTGTGTGTGT 2280  
QY 2281 CCGCCACCGAATCTGACGCAATGCTGCAATATAGCCAGCAAGATGCGCGGGG 2340  
DB 2281 CCGCCACCGAATCTGACGCAATGCTGCAATATAGCCAGCAAGATGCGCGGGG 2340  
QY 2341 ATGCTACTGCGGCTCCAGCACTTGTGTGACACCGGATTTTGGCCACCAAGAACTGCTG 2400  
DB 2341 ATGCTACTGCGGCTCCAGCACTTGTGTGACACCGGATTTTGGCCACCAAGAACTGCTG 2400  
QY 2401 GTGCGGAGAACTTGTGTGAAATCGGGGACTTTTGGATGTCTCCGGAGCTGTACAGC 2460  
DB 2401 GTGCGGAGAACTTGTGTGAAATCGGGGACTTTTGGATGTCTCCGGAGCTGTACAGC 2460  
QY 2461 ACTGACTACTACAGGCTCGGTGGCCACCAATGCTGCCATTTGCTGTGATGCTTCCAGAG 2520  
DB 2461 ACTGACTACTACAGGCTCGGTGGCCACCAATGCTGCCATTTGCTGTGATGCTTCCAGAG 2520  
QY 2521 AGCATCATGTACAGAAATTCAGACGGAAAGGACGCTGTGAGCCTGGGGGTCTGTG 2580  
DB 2521 AGCATCATGTACAGAAATTCAGACGGAAAGGACGCTGTGAGCCTGGGGGTCTGTG 2580  
QY 2581 TGGGAGATTTTCACTATGGCAACAGCCCTGGTACAGGCTGTCAACATGAGGTGATA 2640  
DB 2581 TGGGAGATTTTCACTATGGCAACAGCCCTGGTACAGGCTGTCAACATGAGGTGATA 2640  
QY 2641 GAGTGTATCACTCAGGGCCGAGTCTGTGACGCAACCCGACAGTGGCCCGAGAGTGTAT 2700  
DB 2641 GAGTGTATCACTCAGGGCCGAGTCTGTGACGCAACCCGACAGTGGCCCGAGAGTGTAT 2700  
QY 2701 GAGCTGATGTGGGGTGTGTGACGGAGAGCCCAATGAGAAACATCAAGGGATC 2760  
DB 2701 GAGCTGATGTGGGGTGTGTGACGGAGAGCCCAATGAGAAACATCAAGGGATC 2760  
QY 2761 CATACCTCCTTGAGAACTTGGCAAGGACATCTCCGCTTCACTGTGACATTTAGGCTAG 2820  
DB 2761 CATACCTCCTTGAGAACTTGGCAAGGACATCTCCGCTTCACTGTGACATTTAGGCTAG 2820  
QY 2821 GGCCCTTTTCCCAAGCCGATCTTCCCAAGTACTCTTCAAGAGGCTGAGAGATGAA 2880  
DB 2821 GGCCCTTTTCCCAAGCCGATCTTCCCAAGTACTCTTCAAGAGGCTGAGAGATGAA 2880  
QY 2881 CATCTTTTAACTGCGCTGAGAGCCACCAAGCTGTCTCTTCACTGTGACATTTAAC 2940  
DB 2881 CATCTTTTAACTGCGCTGAGAGCCACCAAGCTGTCTCTTCACTGTGACATTTAAC 2940  
QY 2941 ATCAAGACCTCGAGAAAGCTCTGAGGGAGAGGTGTACTTCTTCACTATAGACACA 3000  
DB 2941 ATCAAGACCTCGAGAAAGCTCTGAGGGAGAGGTGTACTTCTTCACTATAGACACA 3000  
QY 3001 GATATGACTCTTTTGGCAATATCTCTTCTCTTTCATCTCCCTTGTGTGTCTT 3060  
DB 3001 GATATGACTCTTTTGGCAATATCTCTTCTCTTTCATCTCCCTTGTGTGTCTT 3060  
QY 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
DB 3061 TTTCTTTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3120  
QY 3121 ACCCTTCTTTGAATCAATGCGCTTGTGATTAATTAATCTGTGATGACAAAGGC 3180  
DB 3121 ACCCTTCTTTGAATCAATGCGCTTGTGATTAATTAATCTGTGATGACAAAGGC 3180  
QY 3181 CTTAACAAAGTATTTTATATACAGACACTCCAGTTTGGCCACCACTAACAA 3240  
DB 3181 CTTAACAAAGTATTTTATATACAGACACTCCAGTTTGGCCACCACTAACAA 3240  
QY 3241 TGCTTGTGTATCTCTGCTTTGATGTGATGAAAAAGGAAAAAATAATTTCACT 3300

Db 3241 TGCCTGTGTGATTCCTGCTTGTATGATGATAAAAAAGGAAAAAANAATATTCTACT 3300  
Qy 3301 TAAACCTTGTCACTTGTCTGTACAGATATGAGAGATTTCTATGATTCACCTTATTTA 3360  
Db 3301 TAAACCTTGTCACTTGTCTGTACAGATATGAGAGATTTCTATGATTCACCTTATTTA 3360  
Qy 3361 TTTATTTATTTATTTACTGTTTCTTATTTGTTTTGGATGCGCTTAAGCCTGTGTATAAAAAGAA 3420  
Db 3361 TTTATTTATTTATTTACTGTTTCTTATTTGTTTTGGATGCGCTTAAGCCTGTGTATAAAAAGAA 3420  
Qy 3421 AACTGTGTTCAATCTGTGAAGCCTTTATCTATGAGATTTAAACCAAGAGAAAAAGAG 3480  
Db 3421 AACTGTGTTCAATCTGTGAAGCCTTTATCTATGAGATTTAAACCAAGAGAAAAAGAG 3480  
Qy 3481 ATTATTTATGAACCGCAATATGGAGAGAACAAAGACCACTGGATTCAGCTGTGTCA 3540  
Db 3481 ATTATTTATGAACCGCAATATGGAGAGAACAAAGACCACTGGATTCAGCTGTGTCA 3540  
Qy 3541 GTCCCTACTTGAAGAAATCTCAGCAACTGTTAGCTGGAGAAATGTATTCGGACCTTCC 3600  
Db 3541 GTCCCTACTTGAAGAAATCTCAGCAACTGTTAGCTGGAGAAATGTATTCGGACCTTCC 3600  
Qy 3601 CCTGAGACCTTTCTGAGAGATAAAAGACTACTGCGCTCTGTGCCATGATGATTCCTT 3660  
Db 3601 CCTGAGACCTTTCTGAGAGATAAAAGACTACTGCGCTCTGTGCCATGATGATTCCTT 3660  
Qy 3661 TCCCATACCAAGAAATATGATGCGTGCAGTAGAGAGAAAGATGGCTT 3707  
Db 3661 TCCCATACCAAGAAATATGATGCGTGCAGTAGAGAGAAAGATGGCTT 3707

RESULT 8  
ABX76428

ID ABX76428 standard; DNA; 4057 BP.

XX AC ABX76428;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polynucleotide #292.

XX KM Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;  
XX KM antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;  
XX KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
XX KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
XX KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US012476.

XX PR 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0280492P.

XX PR 09-NOV-2001; 2001US-0339245P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 29-NOV-2001; 2001US-0334370P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PT Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX DR P-PSDB; ABUS6699.

PT Detecting a lung cancer-associated transcript in a cell from a patient  
PT for treating lung cancer, by contacting a biological sample from the  
PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer.  
XX  
XX Claim 22; Page 418; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridises  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung cancer-  
CC associated polynucleotides and polypeptides are used for identifying a  
CC compound that modulates a lung cancer-associated polypeptide, for  
CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
CC cancer in a patient and for treating a mammal having lung cancer by  
CC administering a modulatory compound identified. The methods are useful  
CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hyperreactivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
CC invention

XX Sequence 4057 BP; 1013 A; 1033 C; 1014 G; 997 T; 0 U; 0 Other;

XX SQ

Query Match 98.4%; Score 3649; DB 8; Length 4057;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 3707; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

Qy 1 CCCCATTTCGATCTTAACAAGAAATCTGCGCCCGAGAGATCCCGACGCGCGGTCGG 60  
Db 132 CCCCATTTCGATCTTAACAAGAAATCTGCGCCCGAGAGATCCCGACGCGCGGTCGG 191

Qy 61 TGCCTGGCG 120  
Db 192 TGCCTGGCG 251

Qy 121 CCCCCTGTAAGCGGTTGCGTATGCGCGGACCACTGTGAACCTTGCGCGCGCGGAAACA 180  
Db 252 CCCCCTGTAAGCGGTTGCGTATGCGCGGACCACTGTGAACCTTGCGCGCGCGGAAACA 311

Qy 181 CTTTCCTCCCGACCACTCAAGCTCTGTAAAGCTGAGTCCGACGCGCGCAACAGC 240  
Db 312 CTTTCCTCCCGACCACTCAAGCTCTGTAAAGCTGAGTCCGACGCGCGCAACAGC 371

Qy 241 ACCGAGAGTTTAAAGAGCGCGCAAGCGCGAAAGGCTCCCGCACGCGTGGGAAAG 300  
Db 372 ACCGAGAGTTTAAAGAGCGCGCAAGCGCGAAAGGCTCCCGCACGCGTGGGAAAG 431

Qy 301 CGGCGGTTGACGCGCGGGAACAAGCACTCGGGCTGCGACTGCGTAAAGATGCTGCC 360  
Db 432 CGGCGGTTGACGCGCGGGAACAAGCACTCGGGCTGCGACTGCGTAAAGATGCTGCC 491

Qy 361 TGGATAAGTGGACATGAGACCGCATGCGCGCTTGCGGCGCTTCTGCTGCTGTTG 420  
Db 492 TGGATAAGTGGACATGAGACCGCATGCGCGCTTGCGGCGCTTCTGCTGCTGTTG 551

Qy 421 GGGCTTGAAGGCGCGCTTTCGCTGCTCCACGCTCTGCAATGCAATGCTCTCGATC 480  
Db 552 GGGCTTGAAGGCGCGCTTTCGCTGCTCCACGCTCTGCAATGCAATGCTCTCGATC 611

Qy 481 TGGTGAAGGACCGCTTTCGCTGCTGCAATGCGCAATTCGGAATGGAGCTTAAGAGTA 540  
Db 612 TGGTGAAGGACCGCTTTCGCTGCTGCAATGCGCAATTCGGAATGGAGCTTAAGAGTA 671

Qy 541 GATCTGAGAAATCAACCGAAATTTTCATGCAAAACGAGAAAGTTAGAAATCATCAAC 600  
Db 672 GATCTGAGAAATCAACCGAAATTTTCATGCAAAACGAGAAAGTTAGAAATCATCAAC 731

Qy 601 GAAGATGATGTTGAAGCTTATGTTGAGCTGAGAAATCTGCAATTTGATTCGATTTA 660  
Db 732 GAAGATGATGTTGAAGCTTATGTTGAGCTGAGAAATCTGCAATTTGATTCGATTTA 791



OY	661	AAATTTGGGCTCATPAAGCATTTTCTGAAAAACGCAACTTGACGACATCAATTTTACC	720
Db	792	AAATTTGGGCTCATPAAGCATTTTCTGAAAAACGCAACTTGACGACATCAATTTTACC	851
OY	721	CGAAACAACTGACGAGTTGTCTTGAGAAACATTTTCGGCACTTGACCTGTGTGTAACCG	780
Db	852	CGAAACAACTGACGAGTTGTCTTGAGAAACATTTTCGGCACTTGACCTGTGTGTAACCG	911
OY	781	ATCTGTGTGGCAATCCATTTTACATGCTCTGTGACATTAATGTGATCAAGACTCTCCAA	840
Db	912	ATCTGTGTGGCAATCCATTTTACATGCTCTGTGACATTAATGTGATCAAGACTCTCCAA	971
OY	841	GAGGCTTAATCCAGTTCGACGACCTACGAGATTGTGATCTGCTGAATGAAGACGAAGAAT	900
Db	972	GAGGCTTAATCCAGTTCGACGACCTACGAGATTGTGATCTGCTGAATGAAGACGAAGAAT	103
OY	901	ATTCCCTGGCAACCTGACAGTACCCTAATTTGTGTTTGGCATTTGCAAACTTGGCCCGA	960
Db	1032	ATTCCCTGGCAACCTGACAGTACCCTAATTTGTGTTTGGCATTTGCAAACTTGGCCCGA	109
OY	961	CCTAACTCACTGTGAGAGAAAGAAAGTCTATCACTTAATCTGTAGTGTGGCAGGTGAT	1021
Db	1092	CCTAACTCACTGTGAGAGAAAGAAAGTCTATCACTTAATCTGTAGTGTGGCAGGTGAT	115
OY	1021	CCGGTTCCTAATATGTAATTGGAGTGTGTGTAACCTGTGTTCCAAACATATGATGAACA	1081
Db	1152	CCGGTTCCTAATATGTAATTGGAGTGTGTGTAACCTGTGTTCCAAACATATGATGAACA	121
OY	1081	AGCCACACACAGGGCTCCTTAAGATTAATACTAATTCATCCGATGACGTGGAAAGCAG	1144
Db	1212	AGCCACACACAGGGCTCCTTAAGATTAATACTAATTCATCCGATGACGTGGAAAGCAG	127
OY	1141	ATCTCTTGTTGTGGCGGAAATCTTGTAAGAGAAAGATCAAGATTCTGTCAACTCACTGAG	1201
Db	1272	ATCTCTTGTTGTGGCGGAAATCTTGTAAGAGAAAGATCAAGATTCTGTCAACTCACTGAG	133
OY	1201	CATTTTGGACCAACTATCAATTTCTGCAATCTCCAACTCGACCAACCACTGTGTGCATT	1261
Db	1332	CATTTTGGACCAACTATCAATTTCTGCAATCTCCAACTCGACCAACCACTGTGTGCATT	139
OY	1261	CCATTTCATCTGTGAAAAGGCAACCCCAACCAAGGCTTCAAGTGTCTATTAACGGGGCAATA	1321
Db	1392	CCATTTCATCTGTGAAAAGGCAACCCCAACCAAGGCTTCAAGTGTCTATTAACGGGGCAATA	145
OY	1321	TTGAATGAGTCCAAATPATCATCTGTACTAATAATACATGTTACCAATGACACGAGATACCA	1381
Db	1452	TTGAATGAGTCCAAATPATCATCTGTACTAATAATACATGTTACCAATGACACGAGATACCA	151
OY	1381	GGCTGCTTCACAGCTGATATATCCCACTCACTGAAACAATGGGGACCTACACTCTAATAGCC	1441
Db	1512	GGCTGCTTCACAGCTGATATATCCCACTCACTGAAACAATGGGGACCTACACTCTAATAGCC	157
OY	1441	AAGAAATGAGTATGGAGAGATGAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTTGA	1501
Db	1572	AAGAAATGAGTATGGAGAGATGAGAAACAGATTTCTGCTCACTTCAATGGGCTGGCTTGA	163
OY	1501	ATTGACGATGTGTGCAAAACCCCAATTAATCTGTATGTATTTATGAAAGATTAATGAACTGCA	1561
Db	1632	ATTGACGATGTGTGCAAAACCCCAATTAATCTGTATGTATTTATGAAAGATTAATGAACTGCA	169
OY	1561	GCGAATGACATGGGGGACACACGAAACAGAAAGTAATGAATCCCTTCCACAGACGTCACT	1621
Db	1692	GCGAATGACATGGGGGACACACGAAACAGAAAGTAATGAATCCCTTCCACAGACGTCACT	175
OY	1621	GATATAAACCGGTGCGGAAACATCTTCGGCTATAGCTGTGTGTGATTCGCTGTGTGATG	1781
Db	1752	GATATAAACCGGTGCGGAAACATCTTCGGCTATAGCTGTGTGTGATTCGCTGTGTGATG	181
OY	1681	GGAATTTTGCTTTTGGTATATGCTGTGTTCTGTGTTAAGTTGGACAGACATCCAAAGTTTGGC	1744
Db	1812	GGAATTTTGCTTTTGGTATATGCTGTGTTCTGTGTTAAGTTGGACAGACATCCAAAGTTTGGC	187

[illegible]



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Db 2952 CAGAACTTGGCCAGAGGCAATCCGCTTCACTGAGCATTTAGGCTAGGCGCTTTTCC 3011
Qy 2933 CAGACCGATCCCTCCCAAGTACTCTCTCAGAGGGGCTGAGAGATGAACATCTTTAACT 2892
Db 3012 CAGACCGATCCCTCCCAAGTACTCTCTCAGAGGGGCTGAGAGATGAACATCTTTAACT 3071
Qy 2893 GCGCGTGGAGGCAACAAGCTGCTCTCCTTCACTCTGACAGTATTACATCAAAAGACTCC 2952
Db 3072 GCGCGTGGAGGCAACAAGCTGCTCTCCTTCACTCTGACAGTATTACATCAAAAGACTCC 3131
Qy 2953 GAGAACTCTGAGGGAAGCAGTGTGACTTTCTTATCATAGACAGTATTGACTCT 3012
Db 3132 GAGAACTCTGAGGGAAGCAGTGTGACTTTCTTATCATAGACAGTATTGACTCT 3191
Qy 3013 TTTGGGCAATATCTCTCTCTTTCATCTCCCTGGTGGTGGTCTTTCTTTTCTT 3072
Db 3192 TTTGGGCAATATCTCTCTCTTTCATCTCCCTGGTGGTGGTCTTTCTTTTCTT 3251
Qy 3073 AATTTCTTTTCTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3132
Db 3252 AATTTCTTTTCTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3311
Qy 3133 GAATCAATCTGGCTTCTGATTAATTAATCTGATGACAAAGGCTTAAACAAGCT 3192
Db 3312 GAATCAATCTGGCTTCTGATTAATTAATCTGATGACAAAGGCTTAAACAAGCT 3371
Qy 3193 AATTTGATATACAGACAGACTCCAGTTGGCCACCAACTAAACATGCTGTTGTA 3252
Db 3372 AATTTGATATACAGACAGACTCCAGTTGGCCACCAACTAAACATGCTGTTGTA 3431
Qy 3253 TTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3312
Db 3432 TTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3491
Qy 3313 CTCTGCTGTAAGATATGAGAGTTCTATGATTAATCTTATTTATTTATTTATTT 3372
Db 3492 CTCTGCTGTAAGATATGAGAGTTCTATGATTAATCTTATTTATTTATTTATTT 3551
Qy 3373 ACCTGCTTATTTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3432
Db 3552 ACCTGCTTATTTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3611
Qy 3433 ATCTGTGAAGCCTTATCTATGAGGATTTAAACAGAGAAAGAAATTTATTTATGA 3492
Db 3612 ATCTGTGAAGCCTTATCTATGAGGATTTAAACAGAGAAAGAAATTTATTTATGA 3671
Qy 3493 CCGCAATATGAGGAAACAAGCAACCACTGGATCAGCTGTGTCAGTCCCTTACTT 3552
Db 3672 CCGCAATATGAGGAAACAAGCAACCACTGGATCAGCTGTGTCAGTCCCTTACTT 3731
Qy 3553 GAAATATCTCAGCACTGTTAGTGGGAAGATGATTTGGGCACTTCCCTGAGAGACT 3612
Db 3732 GAAATATCTCAGCACTGTTAGTGGGAAGATGATTTGGGCACTTCCCTGAGAGACT 3791
Qy 3613 TCTGAGAGTAAAGAAAGAACTAGTGGCTCTGTGCCATGATGATTTCTTTCCATCAG 3672
Db 3792 TCTGAGAGTAAAGAAAGAACTAGTGGCTCTGTGCCATGATGATTTCTTTCCATCAG 3851
Qy 3673 AAATGATAGCGTGCAGTGAAGAGCAAAAGATGCTT 3707
Db 3852 AAATGATAGCGTGCAGTGAAGAGCAAAAGATGCTT 3886

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RESULT 9  
ADN39077  
ID ADN39077 standard; cDNA; 4057 BP.

ADN39077;  
17-JUN-2004 (first entry)  
Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:395.

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XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX Homo sapiens.
XX WO2003042661-A2.
XX 22-MAY-2003.
XX 13-NOV-2002; 2002WO-US036810.
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0343393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-0355250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-0368809P.
XX 04-APR-2002; 2002US-0370110P.
XX 12-APR-2002; 2002US-0371246P.
XX 05-JUN-2002; 2002US-0386141P.
XX 16-JUN-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397775P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevez PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
XX P-PSDB; ADN39078.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX Claim 8; SEQ ID NO 395; 1385bp; English.
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 4057 BP; 1013 A; 1033 C; 1014 G; 997 T; 0 U; 0 Other;

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Query Match 98.4%; Score 3649; DB 11; Length 4057;  
Best Local Similarity 98.7%; Pred. NO. 0;  
Matches 3707; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

OY	1	CCCCATTGCGATCTTAACAAGGAATCTGCGCCCGAGAGATGCCGCGCGCGTTCGG	60
Db	132	CCCCATTGCGATCTTAACAAGGAATCTGCGCCCGAGAGATGCCGCGCGTTCGG	191
OY	61	TGCCCGGCGCGCGCGCGCATGACGGAGAGCGCGCGCGGAGCTCCGACACGGGTAGCGC	120
Db	192	TGCCCGGCGCGCGCGCGCATGACGGAGAGCGCGCGCGGAGCTCCGACACGGGTAGCGC	251
OY	121	CCCCCTGTAAAGCGGTGTGCTATGCGCGGAGACCATCTGTAAACCTTCGCCCTGCCGAGACA	180
Db	252	CCCCCTGTAAAGCGGTGTGCTATGCGCGGAGACCATCTGTAAACCTTCGCCCTGCCGAGACA	311
OY	181	CTCTTCGCTCCGGACCGAGCTAGACCTCTGATTAAGTGGACTTCGAGCAGCCCGACAAAGC	240
Db	312	CTCTTCGCTCCGGACCGAGCTAGACCTCTGATTAAGTGGACTTCGAGCAGCCCGACAAAGC	371
OY	241	ACCGAGGAGTTTAAGAGCGCCGACACGGAGGGAAGGCTCCCGGACGGGTGGGGAAAG	300
Db	372	ACCGAGGAGTTTAAGAGCGCCGACACGGAGGGAAGGCTCCCGGACGGGTGGGGAAAG	431
OY	301	CGGCGCGGTGACAGCGCGGGACAGGACCTCGGGCTGGCACTGGCTGTAGAGATGTGCTC	360
Db	432	CGGCGCGGTGACAGCGCGGGACAGGACCTCGGGCTGGCACTGGCTGTAGAGATGTGCTC	491
OY	361	TGGATTAAGGTGGACTGAAACCGCGCATGCGCGGCTCTGGGCGCTTCTGCTGGCTGGTGTG	420
Db	492	TGGATTAAGGTGGACTGAAACCGCGCATGCGCGGCTCTGGGCGCTTCTGCTGGCTGGTGTG	551
OY	421	GGCTTCTGAGAGGCGCGCTTTCGCTGTCCACGTCCTGCGAAATGCAAGTGCCTTCGATC	480
Db	552	GGCTTCTGAGAGGCGCGCTTTCGCTGTCCACGTCCTGCGAAATGCAAGTGCCTTCGATC	611
OY	481	TGGTGCAGCGACCCCTTCTCCTGGACCTGCGGATTTCCGAGATTGGAGCCTTAACAGTGA	540
Db	612	TGGTGCAGCGACCCCTTCTCCTGGACCTGCGGATTTCCGAGATTGGAGCCTTAACAGTGA	671
OY	541	GATCCTGAGAACATCAACCGAAATTTTCAATCGCAACCGAAAGGTTTGAATAATCATCAAC	600
Db	672	GATCCTGAGAACATCAACCGAAATTTTCAATCGCAACCGAAAGGTTTGAATAATCATCAAC	731
OY	601	GAAATGATGTTGAAGCTTATGTGGGACTGAGAAATCTGACAAATTGTGGATTCTGGAATTA	660
Db	732	GAAATGATGTTGAAGCTTATGTGGGACTGAGAAATCTGACAAATTGTGGATTCTGGAATTA	791
OY	661	AAATTGTGGCTCATTAAGACATTTCTGAAAAACAGCAACCTGCAGCAATCAATTTTACC	720
Db	792	AAATTGTGGCTCATTAAGACATTTCTGAAAAACAGCAACCTGCAGCAATCAATTTTACC	851
OY	721	CGAAACAACTGACGAGATTGTCTAGAAACATTTCCGTCAACTTGACTTGTCTGAACGTG	780
Db	852	CGAAACAACTGACGAGATTGTCTAGAAACATTTCCGTCAACTTGACTTGTCTGAACGTG	911
OY	781	ATCTCGTGGGCGATCCATTTACATGCTCTGTGACATTAATGTGGATCAAGACTCTCCAA	840
Db	912	ATCTCGTGGGCGATCCATTTACATGCTCTGTGACATTAATGTGGATCAAGACTCTCCAA	971
OY	841	GAGGCTAATCAGTCAGACGACCTCAGAAATTTGTATCTGCTGAATGAAGAAGCAAGAT	900
Db	972	GAGGCTAATCAGTCAGACGACCTCAGAAATTTGTATCTGCTGAATGAAGAAGCAAGAT	1031
OY	901	ATTCCCTGCGCAAACTGCGAGATACCCAAATTGTGGTTGGCATCTGCAAAATCTGGCGCA	960
Db	1032	ATTCCCTGCGCAAACTGCGAGATACCCAAATTGTGGTTGGCATCTGCAAAATCTGGCGCA	1091
OY	961	CCTTAACCTCACTGTGGAGAGAAAGTCTATCACTTATCCTGTAGTGTGGCAGGTGAT	1020
Db	1092	CCTTAACCTCACTGTGGAGAGAAAGTCTATCACTTATCCTGTAGTGTGGCAGGTGAT	1151
OY	1021	CGGTTCTCTAATATCTAATTGGGATGTGTGTAACTCGGTTTCCAAACATATTAATGAACA	1080
Db	1152	CGGTTCTCTAATATATGTATTTGGGATGTGTGTAACTCGGTTTCCAAACATATTAATGAACA	1211

QY	1081	AGCCACACACAGGGCTCCTTAAGGATACCTAACATTTTCATTCGGATGACAGTGGGAAGAC	1140
DB	1212	AGCCACACACAGGGCTCCTTAAGGATACCTAACATTTTCATTCGGATGACAGTGGGAAGAC	1271
QY	1141	ATCTCTTGAGGGGGAAAAATCTTGTGTGAGGAGAGATGACAGTTCGTGCAACCTTCACCTGTG	1200
DB	1272	ATCTCTTGAGGGGGAAAAATCTTGTGTGAGGAGAGATGACAGTTCGTGCAACCTTCACCTGTG	1331
QY	1201	CATTTCGACCCAACTATACATTTCTGGAATCTTCACCACTCAGACCCACCACTGTGTGATTT	1260
DB	1332	CATTTCGACCCAACTATACATTTCTGGAATCTTCACCACTCAGACCCACCACTGTGTGATTT	1391
QY	1261	CCATTCACTGTGAAAGGCAACCCCAAAACGAGCGTTGAGTGGTTCTTAAACGGGGCATA	1320
DB	1392	CCATTCACTGTGAAAGGCAACCCCAAAACGAGCGTTGAGTGGTTCTTAAACGGGGCATA	1451
QY	1321	TTGAATAGTCCAAATACATCTGTACTAAATACATTTATCCATGCAATCAGAGAGTACAC	1380
DB	1452	TTGAATAGTCCAAATACATCTGTACTAAATACATTTATCCATGCAATCAGAGAGTACAC	1511
QY	1381	GGCTGCTCCAGCTGATTAATCCCACTCAGATGAAACATGGGAGCTACACTTAATAGCC	1440
DB	1512	GGCTGCTCCAGCTGATTAATCCCACTCAGATGAAACATGGGAGCTACACTTAATAGCC	1571
QY	1441	AAGAATAGATGTGGAAAGATGAGAAACAATTTCTGTCTCATTTAGGGCTGGCTTGA	1500
DB	1572	AAGAATAGATGTGGAAAGATGAGAAACAATTTCTGTCTCATTTAGGGCTGGCTTGA	1631
QY	1501	ATTGACGATGGTGGAAACCCAAATATACCGTAGTATTTATGAAAGTTATGGAACCTGCA	1560
DB	1632	ATTGACGATGGTGGAAACCCAAATATACCGTAGTATTTATGAAAGTTATGGAACCTGCA	1691
QY	1561	GCGAATGACATCGGGGACACCCAGCAAGAAAGTAAATATCCCTTCACAGACGTCAC	1620
DB	1692	GCGAATGACATCGGGGACACCCAGCAAGAAAGTAAATATCCCTTCACAGACGTCAC	1751
QY	1621	GATPAAAAACCGGTGGGAAACATCTCTCGGTCTATGCTGTGGTGGTGAATTGGTGGTGGTG	1680
DB	1752	GATPAAAAACCGGTGGGAAACATCTCTCGGTCTATGCTGTGGTGGTGAATTGGTGGTGGTG	1811
QY	1681	GGATTTTGGCTTTTGTGTAATGCTGTTTCTGTCTTAATGTGGCAAGACATCCAAATTTGGC	1740
DB	1812	GGATTTTGGCTTTTGTGTAATGCTGTTTCTGTCTTAATGTGGCAAGACATCCAAATTTGGC	1871
QY	1741	ATGAAA-----GGGCCA	1752
DB	1872	ATGAAAAGATTCTCATGTTTGGATTTGGGAAAGTAAATACAGACAAAGTGTGGGCCCA	1931
QY	1753	GCTTCGGTATACGAATGATGATGACTCTGCCAGGCCACTCATCATCTCCAAATGGG	1812
DB	1932	GCTTCGGTATACGAATGATGATGACTCTGCCAGGCCACTCATCATCTCCAAATGGG	1991
QY	1813	AGTAACACTCATTTTCTTGGGAAAGGTGGCCAGATGCTGTCAATTATGGAAATGACCAAG	1872
DB	1992	AGTAACACTCATTTTCTTGGGAAAGGTGGCCAGATGCTGTCAATTATGGAAATGACCAAG	2051
QY	1873	ATCCCTGATATGAAAAATCCCAAGTACTTTGGCATCAACAAGTCAAGTCAAGCCAGAC	1932
DB	2052	ATCCCTGATATGAAAAATCCCAAGTACTTTGGCATCAACAAGTCAAGTCAAGCCAGAC	2111
QY	1933	ACATTTGTTGACGACATCAAGCGACATATACATTTGTTGTGAAAAAGGAGCTTAGCGGAAGA	1992
DB	2112	ACATTTGTTGACGACATCAAGCGACATATACATTTGTTGTGAAAAAGGAGCTTAGCGGAAGA	2171
QY	1993	GCTTTTGGAAAAAGTGTCTTAAGCTGAATGCTATTAACCTCTGTCTGTGACGACGACAGATC	2052
DB	2172	GCTTTTGGAAAAAGTGTGTCTTAAGCTGAATGCTATTAACCTCTGTCTGTGACGACGACAGATC	2231
QY	2053	TTGGTGGCAGGAAGACCTCGAAGGATGCGACAGTGAACAATCAAGCAAGGACCTTCAACCGT	2112
DB	2232	TTGGTGGCAGGAAGACCTCGAAGGATGCGACAGTGAACAATCAAGCAAGGACCTTCAACCGT	2291
QY	2113	GAGGCCAGAGCTCTGACCAACTTCACAGATGAGCAATCGTCAAGTTCATATGGCGTCTGC	2172

Db 2292 GAGGCCAGGCTCCGACCAACCTCCAGCATGAGCACAATGCTCAAGTTCTATGGGTCTGCG 2351  
 Qy 2173 GTGGAGGCGGACCCCTCATCATGATGTTGAGTACATGAAAGATGAGGAGCTCAACAG 2232  
 Db 2352 GTGGAGGCGGACCCCTCATCATGATGTTGAGTACATGAAAGATGAGGAGCTCAACAG 2411  
 Qy 2233 TTCTCTGAGGACACAGGCGCCCTGATGCGGTGCTGATGAGGAGCAACCCGCCACGAA 2292  
 Db 2412 TTCTCTGAGGAGACAGGCGCCCTGATGCGGTGCTGATGAGGAGCAACCCGCCACGAA 2471  
 Qy 2293 CTGACGAGTGTGAGATGCTGATATAGCCAGACAGATGCGCGGCGAGATGCTTACCTG 2352  
 Db 2472 CTGACGAGTGTGAGATGCTGATATAGCCAGACAGATGCGCGGCGAGATGCTTACCTG 2531  
 Qy 2253 GCGGCCAGACCTTGCGACCGGATTTGGCCACAGAACTGCGCTGTCGGGAGAAC 2412  
 Db 2532 GCGGCCAGACCTTGCGACCGGATTTGGCCACAGAACTGCGCTGTCGGGAGAAC 2591  
 Qy 2413 TTGCTGTGAAAATCGGGGACTTTGGGATGTCGGGAGCTGTACAGCACTGACTATAC 2472  
 Db 2592 TTGCTGTGAAAATCGGGGACTTTGGGATGTCGGGAGCTGTACAGCACTGACTATAC 2651  
 Qy 2473 AGGATGCTGCGCACACAAATGCTGCCATTCGCTGATGCTCCAGAGAGCATGATAC 2532  
 Db 2652 AGGATGCTGCGCACACAAATGCTGCCATTCGCTGATGCTCCAGAGAGCATGATAC 2711  
 Qy 2533 AGGAAATTCACAGAGGAAAGAGAGCTGAGAGCTGGGGGCTGCTGTTGTGGAGATTTTC 2592  
 Db 2712 AGGAAATTCACAGAGGAAAGAGAGCTGAGAGCTGGGGGCTGCTGTTGTGGAGATTTTC 2771  
 Qy 2593 ACCTATGAGCAACAGCCCTGGTACAGCTGTCAAAACATGAGGAGATAGATGATACCT 2652  
 Db 2772 ACCTATGAGCAACAGCCCTGGTACAGCTGTCAAAACATGAGGAGATAGATGATACCT 2831  
 Qy 2653 CAGGGCCGAGTCTGACGACGACCCCGACGTCGCCGAGAGAGTGTATGAGCTGATGCTG 2712  
 Db 2832 CAGGGCCGAGTCTGACGACGACCCCGACGTCGCCGAGAGAGTGTATGAGCTGATGCTG 2891  
 Qy 2713 GGGTGTCTGACGAGGAGAGCCCAATGAGAAACATCAAGGAGATCCATACCTCTT 2772  
 Db 2892 GGGTGTCTGACGAGGAGAGCCCAATGAGAAACATCAAGGAGATCCATACCTCTT 2951  
 Qy 2773 CAGAACTTGGCCAAAGGATCTCCGGTCACTGAGCAATTCAGAGCTTGGGCGCTTTTCCC 2832  
 Db 2952 CAGAACTTGGCCAAAGGATCTCCGGTCACTGAGCAATTCAGAGCTTGGGCGCTTTTCCC 3011  
 Qy 2833 CAGACGATCTCTCCCAAGTACTCTCAGACGGGCTGAGAGATGAACATCTTTTAACT 2892  
 Db 3012 CAGACGATCTCTCCCAAGTACTCTCAGACGGGCTGAGAGATGAACATCTTTTAACT 3071  
 Qy 2893 GCCGCTGAGAGCCCAAGCTGCTCTCTCTCACTGTGACAGTATTAACATCAAGACTCC 2952  
 Db 3072 GCCGCTGAGAGCCCAAGCTGCTCTCTCTCACTGTGACAGTATTAACATCAAGACTCC 3131  
 Qy 2953 GAGAGGCTCTGAGGAAAGAGTGTACTTCTTCACTCACTGACAGATTAACATCAAGACTCT 3012  
 Db 3132 GAGAGGCTCTGAGGAAAGAGTGTACTTCTTCACTCACTGACAGATTAACATCAAGACTCT 3191  
 Qy 3013 TTTTGGATTAATCTCTTCTCTCTTCACTCCCTGATGCTCTTTTCTTTTCTTTTCTT 3072  
 Db 3192 TTTTGGATTAATCTCTTCTCTCTTCACTCCCTGATGCTCTTTTCTTTTCTTTTCTT 3251  
 Qy 3073 AATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3132  
 Db 3252 AATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3311  
 Qy 3133 GAATCATATGAGGCTTCTGATTAATTAATCTGATTAAGCAAGGCTTAAGAAAGCT 3192  
 Db 3312 GAATCATATGAGGCTTCTGATTAATTAATCTGATTAAGCAAGGCTTAAGAAAGCT 3371  
 Qy 3193 AATTTGTATATGAGACACTCAGTTTGCACACCACTAACTAATGCTGTTGTATA 3252

Db 3372 AATTTGTATATGAGACAGACACTCCAGTTTGTCCCAACCAACTAATGCTGTTGTATA 3431  
 Qy 3253 TTCCTGCTTTGATATGAGATGATAAAGGAAACAAATATTTCACTTAACTTTGCA 3312  
 Db 3432 TTCCTGCTTTGATATGAGATGATAAAGGAAACAAATATTTCACTTAACTTTGCA 3491  
 Qy 3313 CTTCCTGTGATAGATATGAGAGATTTCTATGATTAACCTTCACTTATTTATTTATTT 3372  
 Db 3492 CTTCCTGTGATAGATATGAGAGATTTCTATGATTAACCTTCACTTATTTATTTATTT 3551  
 Qy 3373 ACTGTTCTTATGTTTGTGATGAGCTTAACCTGTGTATTAAGAAACCTGTGTCA 3432  
 Db 3552 ACTGTTCTTATGTTTGTGATGAGCTTAACCTGTGTATTAAGAAACCTGTGTCA 3611  
 Qy 3433 ATCTGTAAACCTTTATCTATGAGATTAACCAAGAGAAAGAGATTTATATGA 3492  
 Db 3612 ATCTGTAAACCTTTATCTATGAGATTAACCAAGAGAAAGAGATTTATATGA 3671  
 Qy 3493 CCGCAATATGAGAGAAACAAAGCAACACTGGAGTACGCTGTGATCCTTACCTTAG 3552  
 Db 3672 CCGCAATATGAGAGAAACAAAGCAACACTGGAGTACGCTGTGATCCTTACCTTAG 3731  
 Qy 3553 GAATATCTCAGCACTGTTAGCTGGAGAAATGATTTCCGACCTTCCCTGAGACCTT 3612  
 Db 3732 GAATATCTCAGCACTGTTAGCTGGAGAAATGATTTCCGACCTTCCCTGAGACCTT 3791  
 Qy 3613 TCTGAGAGTAAAGACTATGAGGCTCTGAGCAATGATTTCCATCACAG 3672  
 Db 3792 TCTGAGAGTAAAGACTATGAGGCTCTGAGCAATGATTTCCATCACAG 3851  
 Qy 3673 AAATGATAGCGTCACTGAGAGAGCAAGATGCTT 3707  
 Db 3852 AAATGATAGCGTCACTGAGAGAGCAAGATGCTT 3886

RESULT 10  
 ADS92943  
 ID ADS92943 standard; cDNA; 4057 BP.  
 AC ADS92943;  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Neurotrophic tyrosine kinase receptor type 2 cDNA.  
 XX  
 KW cytotretatic; gene therapy; human;  
 KW branching morphogenesis modulating agent; MBM agent; gene; ss.  
 OS Homo sapiens.  
 PN W02004037990-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033549.  
 XX  
 PR 23-OCT-2002; 2002US-0420554P.  
 PR 30-DEC-2002; 2002US-0436941P.  
 PA (EXEL-) EXELIXIS INC.  
 PI Plozman GD, Karim PD, Swimmer C, Habeck HA, Koblizek TI,  
 PI Schulte-Werkler S, Langheinrich U, Stott GM, Trowe T, Vogel AM,  
 PI Odenthal JH, Scheel JK, Will TT, Jin Y, Bjerre LM, Hal B,  
 PI Adamkewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;  
 PI Nicoll M;  
 XX  
 DR WPI: 2004-365506/34.  
 DR P-PSDB; ADS92974.  
 XX  
 PT Identifying a candidate branching morphogenesis modulating agent for  
 PT treating cancer comprises contacting the assay system comprising a MBM  
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-

PT biased activity.  
XX  
XX Example 3, SEQ ID NO 14, 179pp; English.  
CC The invention describes a method of identifying a candidate branching  
CC morphogenesis modulating (MBM) agent. The method comprises: providing an  
CC assay system comprising a MBM polypeptide or nucleic acid; contacting the  
CC assay system with a test agent under conditions where the system provides  
CC a reference activity, except for the presence of the test agent; and  
CC detecting a test agent-biased activity of the assay system, where a  
CC difference between the test agent-biased activity and the reference  
CC activity identifies the test agent as a candidate branching morphogenesis  
CC modulating agent. Also described are: a method of modulating branching  
CC morphogenesis in a mammalian cell; and a method for diagnosing a disease  
CC in a patient. The method is useful in identifying a candidate branching  
CC morphogenesis modulating agent for preparing a composition for diagnosing  
CC or treating cancer. This sequence encodes a human branching morphogenesis  
CC modulating (MBM) protein.  
XX  
SQ Sequence 4057 BP, 1013 A, 1033 C, 1014 G, 997 T, 0 U, 0 Other;

Query Match 98.4%; Score 3649; DB 13; Length 4057;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 3707; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

QY 1 CCCCCATTCGATCTTAACAGAAATCTGCGCCCAAGAGTCCCGACGCCCGCGTCCG 60  
DB 132 CCCCCATTCGATCTTAACAGAAATCTGCGCCCAAGAGTCCCGACGCCCGCGTCCG 191  
QY 61 TGCCCGGCGCGCGCGCATGCAAGCAAGCGCGCGCGGAGCTCCGAGCAAGCGGTAGCGC 120  
DB 192 TGCCCGGCGCGCGCGCATGCAAGCAAGCGCGCGCGGAGCTCCGAGCAAGCGGTAGCGC 251  
QY 121 CCCCCTGTAAAGCGGTTGCTATGCGCGGACCACTGTGAACCTTGCCTGCGCGGAA 180  
DB 252 CCCCCTGTAAAGCGGTTGCTATGCGCGGACCACTGTGAACCTTGCCTGCGCGGAA 311  
QY 181 CTCTTCGCTCCGACACAGCTCAGCTCTGATTAAGCTGAGCTCGGACGCGCCGCAACAGC 240  
DB 312 CTCTTCGCTCCGACACAGCTCAGCTCTGATTAAGCTGAGCTCGGACGCGCCGCAACAGC 371  
QY 241 ACCGAGAGATTAAAGAGCGCGCAAGCGGAGAGGCTCCCGCAAGCGGTGGGGAAG 300  
DB 372 ACCGAGAGATTAAAGAGCGCGCAAGCGGAGAGGCTCCCGCAAGCGGTGGGGAAG 431  
QY 301 CGGCGGCTGACGCGCGGAGCAGGCACTCGGCTGAGCACTGCTAGAGGATGTCCTCC 360  
DB 432 CGGCGGCTGACGCGCGGAGCAGGCACTCGGCTGAGCACTGCTAGAGGATGTCCTCC 491  
QY 361 TGGATTAAGTGGCATGGAACCGGCATGCGCGGCTCTGGGGCTTCTGCTGGCTGGTGTG 420  
DB 492 TGGATTAAGTGGCATGGAACCGGCATGCGCGGCTCTGGGGCTTCTGCTGGCTGGTGTG 551  
QY 421 GGCCTTCGAGAGGCGCGCTTTCGCTGCGCCCAAGCTGCGAAATGCAAGTCCCTCGCATC 480  
DB 552 GGCCTTCGAGAGGCGCGCTTTCGCTGCGCCCAAGCTGCGAAATGCAAGTCCCTCGCATC 611  
QY 481 TGGTGCAGCGACCTTCTCTGCGCATGCTGAGCAATTCGAGATTGAGAGCTTAACAGTGA 540  
DB 612 TGGTGCAGCGACCTTCTCTGCGCATGCTGAGCAATTCGAGATTGAGAGCTTAACAGTGA 671  
QY 541 GATCTTGAGAACATCACCGAAATTTTCATGCAAAACGAAAGATTAGAAATCATCAAC 600  
DB 672 GATCTTGAGAACATCACCGAAATTTTCATGCAAAACGAAAGATTAGAAATCATCAAC 731  
QY 601 GAAGATGATGTTGAAGCTTAATGTGGAGCTGAGAAATCTGACAAATTTGAGATTCTGAGTTA 660  
DB 732 GAAGATGATGTTGAAGCTTAATGTGGAGCTGAGAAATCTGACAAATTTGAGATTCTGAGTTA 791  
QY 661 AATTTTGGCTCATTAAGCAATTTCTGAAAAACAGCAACTGACGACATCAATTTTACC 720  
DB 792 AATTTTGGCTCATTAAGCAATTTCTGAAAAACAGCAACTGACGACATCAATTTTACC 851

QY 721 CGAAACAACTGACGAGTTTGTCTAGAGAAACATTTCCGTCACCTTGACTTGTCTGAACTG 780  
DB 852 CGAAACAACTGACGAGTTTGTCTAGAGAAACATTTCCGTCACCTTGACTTGTCTGAACTG 911  
QY 781 ATCTGGTGGGCAATCATATTACATGCTCCTGAGCATTAATGTGATCAAGACTCTCCAA 840  
DB 912 ATCTGGTGGGCAATCATATTACATGCTCCTGAGCATTAATGTGATCAAGACTCTCCAA 971  
QY 841 GAGGCTAAATCCAGTCCAGACACTCAGAGATTGTACTGCTGAAATGAAAGACAGAAAT 900  
DB 972 GAGGCTAAATCCAGTCCAGACACTCAGAGATTGTACTGCTGAAATGAAAGACAGAAAT 1031  
QY 901 ATTCCCTGCGCAAACTGCGAGATACCCCAATGTGGTTTGGCATCTGCAAACTGGCCGCA 960  
DB 1032 ATTCCCTGCGCAAACTGCGAGATACCCCAATGTGGTTTGGCATCTGCAAACTGGCCGCA 1091  
QY 961 CCTAACCTCCTGTGAGAGAAAGAAAGTCAATCAATTAATCCGTAGTGGAGAGGTAT 1020  
DB 1092 CCTAACCTCCTGTGAGAGAAAGAAAGTCAATCAATTAATCCGTAGTGGAGAGGTAT 1151  
QY 1021 CCGGTTCTTAATATGATATGGAGATGTGTGTAAGTCTGGTTTCCAAACATATGAATGAACA 1080  
DB 1152 CCGGTTCTTAATATGATATGGAGATGTGTGTAAGTCTGGTTTCCAAACATATGAATGAACA 1211  
QY 1081 AGCCACACACAGGCTCTCTTAAGATTAACATTAATTCGATGACAGTGGGAAAGCAG 1140  
DB 1212 AGCCACACACAGGCTCTCTTAAGATTAACATTAATTCGATGACAGTGGGAAAGCAG 1271  
QY 1141 ATCTCTTGTGTGCGGAAAACTTGTAGAGAAAGATCAAGATTCTGCAACTCACTGTG 1200  
DB 1272 ATCTCTTGTGTGCGGAAAACTTGTAGAGAAAGATCAAGATTCTGCAACTCACTGTG 1331  
QY 1201 CATTTTGCAACCAATCAATTCATATTCGAAATCTCCAACTCAGACCACTGCTGCAAT 1260  
DB 1332 CATTTTGCAACCAATCAATTCATATTCGAAATCTCCAACTCAGACCACTGCTGCAAT 1391  
QY 1261 CCAATCACTGTGAAGGCAACCCCAACCGGCTTCAAGTGTCTTAATACGGGGCAATA 1320  
DB 1392 CCAATCACTGTGAAGGCAACCCCAACCGGCTTCAAGTGTCTTAATACGGGGCAATA 1451  
QY 1321 TTGAATGAGTCCAAATACATCTGTATCAATTAATCATGTTTCAATCAACGAGAGTACCAC 1380  
DB 1452 TTGAATGAGTCCAAATACATCTGTATCAATTAATCATGTTTCAATCAACGAGAGTACCAC 1511  
QY 1381 GGCCTGCTCCAGCTGATTAATCCCACTCAATGAAACAATGGGAGCTACATCTTAATAGCC 1440  
DB 1512 GGCCTGCTCCAGCTGATTAATCCCACTCAATGAAACAATGGGAGCTACATCTTAATAGCC 1571  
QY 1441 AAGAATGATTAAGGAAAGGATGAGAAACAGATTTCGCTCACTTCATGAGCTGGCTGGA 1500  
DB 1572 AAGAATGATTAAGGAAAGGATGAGAAACAGATTTCGCTCACTTCATGAGCTGGCTGGA 1631  
QY 1501 ATTGACGATGTCGCAAAACCAAAATTAATCCGATGTAATTAATGAAGTTATGGAACCTGCA 1560  
DB 1632 ATTGACGATGTCGCAAAACCAAAATTAATCCGATGTAATTAATGAAGTTATGGAACCTGCA 1691  
QY 1561 GCGAATGACATCGGAGGACACACAGAAACAGAAATGAAATCCCTTCCACAGACGTCACT 1620  
DB 1692 GCGAATGACATCGGAGGACACACAGAAACAGAAATGAAATCCCTTCCACAGACGTCACT 1751  
QY 1621 GATTAACCGGTCGGGAAACATCTCTGCTGCTATGCTGTGATGATGCTGTGCTG 1680  
DB 1752 GATTAACCGGTCGGGAAACATCTCTGCTGCTATGCTGTGATGATGCTGTGCTG 1811  
QY 1681 GAAATTTGCTTTTGGTAATGCTGTTTCTGCTTAAGTTGGCAAGACCTCAAGTTTGGC 1740  
DB 1812 GAAATTTGCTTTTGGTAATGCTGTTTCTGCTTAAGTTGGCAAGACCTCAAGTTTGGC 1871  
QY 1741 ATGAAA-----GGCCCA 1752  
DB 1872 ATGAAAATTTTTCATGCTTTTGGATTTGGGAAAGTAAATCAAGACAGGCTGTGGCCA 1931  
QY 1753 GCCTCGTTATCAGCAATGATGATGACTGTCCAGGCCCACTCATCATCATCTCCAAATGGG 1812

Db 1932 GCGCTCGTTATCAGCAATGATGATGATCTCTCCAGCCCACTCCACATCTCCCAATGCG 1991  
Qy 1813 AGTAACACTCCATCTCTTCGGAAGTGGCCCAAGTGTCTCATTTATGAAATGACCAAG 1872  
Db 1992 AGTAACACTCCATCTCTTCGGAAGTGGCCCAAGTGTCTCATTTATGAAATGACCAAG 2051  
Qy 1873 ATCCCTGTGATTTGAAATATCCCAAGTACTTTGGCATCACCAACAGTCAAGCCAGAC 1932  
Db 2052 ATCCCTGTGATTTGAAATATCCCAAGTACTTTGGCATCACCAACAGTCAAGCCAGAC 2111  
Qy 1933 ACATTTGTTCAGCATTCAGACGACATTAATTTGTTCGAAAAGGAGCTAGGGAGAGA 1992  
Db 2112 ACATTTGTTCAGCATTCAGACGACATTAATTTGTTCGAAAAGGAGCTAGGGAGAGA 2171  
Qy 1993 GCGCTTTGGAAAAGTTCCTAGCTGAATGCTATAACCTGTGCTCCAGACAGACAAAGATC 2052  
Db 2172 GCGCTTTGGAAAAGTTCCTAGCTGAATGCTATAACCTGTGCTCCAGACAGACAAAGATC 2231  
Qy 2053 TTGGTGGCAGTGAAGACCCCTGAAGAGATGCGAGTGAATGCAATGCAAGCAAGACTTCACCGT 2112  
Db 2232 TTGGTGGCAGTGAAGACCCCTGAAGAGATGCGAGTGAATGCAATGCAAGCAAGACTTCACCGT 2291  
Qy 2113 GAGGCCAGACTCTGACCAACCTCCAGATGAGACATCTCAAGTTCTATGGCGTTCG 2172  
Db 2292 GAGGCCAGACTCTGACCAACCTCCAGATGAGACATCTCAAGTTCTATGGCGTTCG 2351  
Qy 2173 GTGAGAGGCGACCCCTCATGATGGCTTTGAGTACATGAAGCANTGGGACCTCAACAG 2232  
Db 2352 GTGAGAGGCGACCCCTCATGATGGCTTTGAGTACATGAAGCANTGGGACCTCAACAG 2411  
Qy 2233 TTCTCTAGGGGACACCGGCCCTGATGCGTGTGAATGGCTGAGGGGCAACCCGCCACGAA 2292  
Db 2412 TTCTCTAGGGGACACCGGCCCTGATGCGTGTGAATGGCTGAGGGGCAACCCGCCACGAA 2471  
Qy 2293 CTGAACGAGTGGCAGATGCTGCATATAGCCAGACAGATGCGCGGGGCAATGCTTACCTG 2352  
Db 2472 CTGAACGAGTGGCAGATGCTGCATATAGCCAGACAGATGCGCGGGGCAATGCTTACCTG 2531  
Qy 2353 GCGGCCAGACCTTCGTGCAACCGGATTTGGCCACCGAACTGCTGGTGGGGAGAAC 2412  
Db 2532 GCGGCCAGACCTTCGTGCAACCGGATTTGGCCACCGAACTGCTGGTGGGGAGAAC 2591  
Qy 2413 TTGCTGTGTAATATCGGGGACTTTGGGATGTCGCGGAGCTGTACAGCACTGACTAC 2472  
Db 2592 TTGCTGTGTAATATCGGGGACTTTGGGATGTCGCGGAGCTGTACAGCACTGACTAC 2651  
Qy 2473 AGGGTCGGTGGCACAACATGCTGCCATTCGTGATGCTCCAGAGAGCATGATAC 2532  
Db 2652 AGGGTCGGTGGCACAACATGCTGCCATTCGTGATGCTCCAGAGAGCATGATAC 2711  
Qy 2533 AGGAAATTCAGACGGAAGGAGAGCTGTGAGCCTGGGGGCTGCTGTGGGAATTTTC 2592  
Db 2712 AGGAAATTCAGACGGAAGGAGAGCTGTGAGCCTGGGGGCTGCTGTGGGAATTTTC 2771  
Qy 2593 ACCTATGSCAAACAGCCCTGTGTACAGCTGTCAACATAGAGTGTAGTATGACT 2652  
Db 2772 ACCTATGSCAAACAGCCCTGTGTACAGCTGTGTCAACATAGAGTGTATGACT 2831  
Qy 2653 CAGGGCCGAGTCTGACAGCAGCCCGCAGCTGCCCCAGAGGTGTATGACTGATGCTG 2712  
Db 2832 CAGGGCCGAGTCTGACAGCAGCCCGCAGCTGCCCCAGAGGTGTATGACTGATGCTG 2891  
Qy 2713 GGGTGTGGCAGCAGAGCCCCCATGAGGAAACATCAAGGGCATTCATACCTCTT 2772  
Db 2892 GGGTGTGGCAGCAGAGCCCCCATGAGGAAACATCAAGGGCATTCATACCTCTT 2951  
Qy 2773 CAGAACTTGGCAGAGGCACTCCGGTCTACCTGACATTTAGAGCTAGAGCCCTTTTCC 2832  
Db 2952 CAGAACTTGGCAGAGGCACTCCGGTCTACCTGACATTTAGAGCTAGAGCCCTTTTCC 3011  
Qy 2833 CAGAACGATCTTCCCAACGTAATCTTCAGACGGGCTGAGAGATGAACATTTTAACT 2892

Db 3012 CAGAACGATCTTCCCAACGTAATCTTCAGACGGGCTGAGAGATGAACATCTTTAACT 3071  
Qy 2893 GCCGCTGAGGCGACCAAGCTGTCTCTCTTCACTCTGACAGTATTTAACATCAAGACTCC 2952  
Db 3072 GCCGCTGAGGCGACCAAGCTGTCTCTCTTCACTCTGACAGTATTTAACATCAAGACTCC 3131  
Qy 2953 GAGAGCTCTGAGGAGAGCAGTGTATCTTTTATTCATCATAGACAGATTTAGCTTCT 3012  
Db 3132 GAGAGCTCTGAGGAGAGCAGTGTATCTTTTATTCATCATAGACAGATTTAGCTTCT 3191  
Qy 3013 TTTTGGCATATCTCTTCTCTCTTTCATCTCCCTGGTGTGTCTTTCTTTTCTT 3072  
Db 3192 TTTTGGCATATCTCTTCTCTCTTTCATCTCCCTGGTGTGTCTTTCTTTTCTT 3251  
Qy 3073 AATTTTCCTTTTCTCTTTTCTTTTCTTCCCTCCAGTCAAGATTTCACTTACCTTCTT 3132  
Db 3252 AATTTTCCTTTTCTCTTTTCTTTTCTTCCCTCCAGTCAAGATTTCACTTACCTTCTT 3311  
Qy 3133 GAATCAATCTGGCTTCTGCAATTAATTAATCTGATAGACAAAGGCTTTAACAAAGCT 3192  
Db 3312 GAATCAATCTGGCTTCTGCAATTAATTAATCTGATAGACAAAGGCTTTAACAAAGCT 3371  
Qy 3193 AATTTGTTATATCAGACGACCTGCAATTTGCCACCACTAACATGCTTGTGTA 3252  
Db 3372 AATTTGTTATATCAGACGACCTGCAATTTGCCACCACTAACATGCTTGTGTA 3431  
Qy 3253 TTCTGCGCTTTGATGTGAGTGAATAAAGGAAACAAATTTTCACTTAACTTTGTA 3312  
Db 3432 TTCTGCGCTTTGATGTGAGTGAATAAAGGAAACAAATTTTCACTTAACTTTGTA 3491  
Qy 3313 CTTCGTGTAACAGATATCAGAGATTTCTATGATTCATTTATTTATTTATTT 3372  
Db 3492 CTTCGTGTAACAGATATCAGAGATTTCTATGATTCATTTATTTATTTATTT 3551  
Qy 3373 ACTGTCTTATTTGTTTTGATGAGCTTAAAGCTGTGTATTAAGAAACCTGTGTA 3432  
Db 3552 ACTGTCTTATTTGTTTTGATGAGCTTAAAGCTGTGTATTAAGAAACCTGTGTA 3611  
Qy 3433 ATCTGTGAAGCTTTATCTATGAGGAGTTAAACAGAGAAAGATTTATTAAGAA 3492  
Db 3612 ATCTGTGAAGCTTTATCTATGAGGAGTTAAACAGAGAAAGATTTATTAAGAA 3671  
Qy 3493 CCGCAATATGAGAGAAACAAAGCAACCTGAGTACGCTGTGATCCTACTTAG 3552  
Db 3672 CCGCAATATGAGAGAAACAAAGCAACCTGAGTACGCTGTGATCCTACTTAG 3731  
Qy 3553 GAAATATCTAGCACTGTATGCTGGAGAAATGTATTCGACCTTCCCTGAGGACCTT 3612  
Db 3732 GAAATATCTAGCACTGTATGCTGGAGAAATGTATTCGACCTTCCCTGAGGACCTT 3791  
Qy 3613 TCTGAGAGTAAAGAAAGCTATCTGGCTCTGTGCCATGAGATTTCTTTCCCATCACAG 3672  
Db 3792 TCTGAGAGTAAAGAAAGCTATCTGGCTCTGTGCCATGAGATTTCTTTCCCATCACAG 3851  
Qy 3673 AAATGATAGCGTGCATGAGAGCAAGATGCTT 3707  
Db 3852 AAATGATAGCGTGCATGAGAGCAAGATGCTT 3886

RESULT 11  
AAT00689  
ID AAT00689 standard; DNA; 3194 BP.  
XX  
AC AAT00689;  
XX  
DT 31-MAR-1996 (first entry)  
XX  
DE Human tkrB receptor DNA.  
XX  
XX tkrB receptor; tyrosine-kinase; enzyme; protease; inflammation; pain;  
KM diagnosis; neurotrophic factor; kidney; lung; psychiatric disorder; 86.  
XX  
OS Homo sapiens.



XX Key Location/Qualifiers  
 FT CDS 114..2582  
 FT /\*tag= 1  
 FT misc\_feature 312..321  
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 FT /note= "potential N-linked glycosylation site"  
 FT 396..407  
 FT /\*tag= b  
 FT /note= "potential N-linked glycosylation site"  
 FT 474..485  
 FT /\*tag= c  
 FT /note= "potential N-linked glycosylation site"  
 FT 645..656  
 FT /\*tag= d  
 FT /note= "potential N-linked glycosylation site"  
 FT 726..737  
 FT /\*tag= e  
 FT /note= "potential N-linked glycosylation site"  
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 FT /note= "potential N-linked glycosylation site"  
 FT 873..884  
 FT /\*tag= g  
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 FT 951..962  
 FT /\*tag= h  
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 FT 1086..1097  
 FT /\*tag= i  
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 FT /note= "potential N-linked glycosylation site"  
 FT 1404..1475  
 FT /\*tag= m  
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 FT 1511  
 FT /\*tag= o  
 FT /note= "splice site for truncated form of trkC"  
 FT 1743..2534  
 FT /\*tag= n  
 FT /note= "tyrosine-kinase domain"  
 XX MO9525795-A1.  
 XX PN  
 XX 28-SEP-1995.  
 XX PD  
 XX 17-MAR-1995; 95MO-US003426.  
 XX PF  
 XX 18-MAR-1994; 94US-00215139.  
 XX PR 05-AUG-1994; 94US-00286846.  
 XX PR 20-DEC-1994; 94US-00359705.  
 XX XX  
 PA (GETH ) GENENTECH INC.  
 XX XX  
 PI Presta LG, Shelton DL, Ufer R;  
 XX XX  
 DR WPI; 1995-344616/44.  
 XX P-PSDB; AAR81630.  
 XX XX  
 PT New human trkB and trkC poly(peptide(s) and fusion proteins contg. them -  
 PT also DNA, vectors and transformed cells useful in treatment and diagnosis  
 PT of abnormal neurotrophic factor expression, e.g. inflammatory pain.  
 XX XX  
 PS Claim 8; Fig 1A-B; 117pp; English.  
 XX XX  
 CC This DNA sequence may be expressed recombinantly for the production of  
 CC human trkC receptor, and to detect or amplify trkC genes. The encoded  
 CC protein may be used as a reagent in kinase receptor activation assays.

CC and therapeutically in diseases associated with over or under expression  
 CC of neurotrophic factor (e.g. pain of inflammation, kidney, lung,  
 CC cardiovascular or psychiatric disorders and some sorts of tumors)  
 XX  
 SQ Sequence 3194 BP; 824 A; 793 C; 761 G; 816 T; 0 U; 0 Other;

Query Match 85.2%; Score 3156.6; DB 2; Length 3194;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 3162; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 252 AAGAGAGCCGCAAGCCAGGAGAGGCTCCCGCAGCGGTGGGGAAGCGCGGTGCA 311  
 DB 14 AAGAGCCGCAAGCCAGGAGAGGCTCCCGCAGCGGTGGGGAAGCGCGGTGCA 73  
 QY 312 GCGCGGGGACAGGCACTCGGCTGGGCACTGGCTGTAGAGATGTCCTGTAAAGTG 371  
 DB 74 GCGCGGGGACAGGCACTCGGCTGGGCACTGGCTGTAGAGATGTCCTGTAAAGTG 133  
 QY 372 GCATGACCCGCGCATGGCGGCTTGGGGCTTGTGTGTGGCTTTGTGAG 431  
 DB 134 GCATGACCCGCGCATGGCGGCTTGGGGCTTGTGTGTGGCTTTGTGAG 193  
 QY 432 GCGCGCTTTCGCTGTCCTGCTCCACGTCCTGCAAAATGCAAGTCTCGATCTGTACGCA 491  
 DB 194 GCGCGCTTTCGCTGTCCTGCTCCACGTCCTGCAAAATGCAAGTCTCGATCTGTACGCA 253  
 QY 492 CCTTCTCTCGCATGCTGATCTTCGAGATTGAGCCCTAACGTAGATCTTGAGAA 551  
 DB 254 CCTTCTCTCGCATGCTGATCTTCGAGATTGAGCCCTAACGTAGATCTTGAGAA 313  
 QY 552 CATCACCAGAAATTTTCATGCGCAACGAGAAAGTTAGAAATCATCAAGAAATGATGT 611  
 DB 314 CATCACCAGAAATTTTCATGCGCAACGAGAAAGTTAGAAATCATCAAGAAATGATGT 373  
 QY 612 TGAAGCTTATGTGGGACTGAGAAATCGAACATTTGATTTGATTTAAATTTTGCG 671  
 DB 374 TGAAGCTTATGTGGGACTGAGAAATCGAACATTTGATTTGATTTAAATTTTGCG 433  
 QY 672 TCATAAAGCATTTCTGAAAAACGAACTGCGACATCATATTTTACCGGAACAACT 731  
 DB 434 TCATAAAGCATTTCTGAAAAACGAACTGCGACATCATATTTTACCGGAACAACT 493  
 QY 732 GACGAGTTGTCTAGGAAACATTTCCGTACCTTGAATCTGTGAATCTCTGTGGG 791  
 DB 494 GACGAGTTGTCTAGGAAACATTTCCGTACCTTGAATCTGTGAATCTCTGTGGG 553  
 QY 792 CAATCATTTACATGCTCCGTGACATTTATGTGATCAAGACTCTCAAGAGGCTAAATC 851  
 DB 554 CAATCATTTACATGCTCCGTGACATTTATGTGATCAAGACTCTCTCAAGAGGCTAAATC 613  
 QY 852 CAGTCGACACTCAGGATTTGTACTGCTGAAATGAAAGCAGCAAGAAATTTCCCTGAG 911  
 DB 614 CAGTCGACACTCAGGATTTGTACTGCTGAAATGAAAGCAGCAAGAAATTTCCCTGAG 673  
 QY 912 AAACCTGAGATACCAATTTGTGTTTGCATCTGCAATCTGCGGACCTTAACCTGAC 971  
 DB 674 AAACCTGAGATACCAATTTGTGTTTGCATCTGCAATCTGCGGACCTTAACCTGAC 733  
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 DB 734 TGTGAGAGAGAGAAAGTCTATCAATTATCTGTAGTGGGAGGTATCCGGTCTTAA 793  
 QY 1032 TATGTATTGGATTTGTGTAACCTGTGTTTCAAAATATATGAAACAGACACACACA 1091  
 DB 794 TATGTATTGGATTTGTGTAACCTGTGTTTCAAAATATATGAAACAGACACACACA 853  
 QY 1092 GGGCTCCTTAAGGATTAATCAATTTTCATCCATGACAGTGGGAGAGATCTTGTGT 1151  
 DB 854 GGGCTCCTTAAGGATTAATCAATTTTCATCCATGACAGTGGGAGAGATCTTGTGT 913  
 QY 1152 GGGGAAAAATCTGTAGAGAAATCAAGATTTGTGTCAACCTCATGTGATTTTGACC 1211  
 DB 914 GGGGAAAAATCTGTAGAGAAATCAAGATTTGTGTCAACCTCATGTGATTTTGACC 973



Qy 1212 AACTATCAATTTCGAAATCTCAACCTCAGACCACTGTGTCAATTCATCACTGT 1271  
Db 974 AACTATCAATTTCTCGAATCTCAACTCAGACCACTGTGTCAATTCATCACTGT 1033  
Qy 1272 GAAAGGCAACCCCAACCAAGGCTTCAGTGGTTCTATTAAGGGGCAATTTGAATGATC 1331  
Db 1034 GAAAGGCAACCCCAACCAAGGCTTCAGTGGTTCTATTAAGGGGCAATTTGAATGATC 1093  
Qy 1332 CAATATCATCTGTCTAATAATCAATGTATACCAATCAGAGGATACAGGGCTGCTCA 1391  
Db 1094 CAATATCATCTGTCTAATAATCAATGTATACCAATCAGAGGATACAGGGCTGCTCA 1153  
Qy 1392 GCTGTATATCCCATCTCAATGAACAATGGGGACTACCTTAATAGCCAATGATGTA 1451  
Db 1154 GCTGTATATCCCATCTCAATGAACAATGGGGACTACCTTAATAGCCAATGATGTA 1213  
Qy 1452 TGGGAAGATGAGAAACAGATTTTCTCTCACTTCAATGGGCTGGCTGGAAATTCAGATGG 1511  
Db 1214 TGGGAAGATGAGAAACAGATTTTCTCTCACTTCAATGGGCTGGCTGGAAATTCAGATGG 1273  
Qy 1512 TGCAAAACCAATTAATCTGTATGTAATTTATGAAGATTATGAAGCTGAGGGAATGAT 1571  
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Qy 1572 CGGGGACACACGAAAGAAATGAATCCCTTCCACAGACGTCACTGAATAAACCGG 1631  
Db 1334 CGGGGACACACGAAAGAAATGAATCCCTTCCACAGACGTCACTGAATAAACCGG 1393  
Qy 1632 TCGGGAACATCTCTCGGTCTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1691  
Db 1394 TCGGGAACATCTCTCGGTCTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1453  
Qy 1692 TTTGTATGCTGT 1751  
Db 1454 TTTGTATGCTGT 1513  
Qy 1752 AGCCCTCGTTATCAGCAATGATGATGATCTGTGCCAGGCCCATCTCAATCTCCATATG 1811  
Db 1514 AGCCCTCGTTATCAGCAATGATGATGATCTGTGCCAGGCCCATCTCAATCTCCATATG 1573  
Qy 1812 GAGTAACTCATCTCTTCTTGTGAAAGTGTGCCAGATGCTGTCAATTAATGAAATGACCA 1871  
Db 1574 GAGTAACTCATCTCTTCTTGTGAAAGTGTGCCAGATGCTGTCAATTAATGAAATGACCA 1633  
Qy 1872 GATCCCTGTCAATTTGAAAATCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1931  
Db 1634 GATCCCTGTCAATTTGAAAATCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1693  
Qy 1932 CACATTTGTGAGCATCAAGCGACATTAATGTTGTGAAAAGGAGCTTAAGGGAAG 1991  
Db 1694 CACATTTGTGAGCATCAAGCGACATTAATGTTGTGAAAAGGAGCTTAAGGGAAG 1753  
Qy 1992 AGCCTTTGAAAAGTGTCTAGCTGATGATGATTAACCTGTCTGTCTGTGAGAGCAAGAT 2051  
Db 1754 AGCCTTTGAAAAGTGTCTAGCTGATGATGATTAACCTGTCTGTCTGTGAGAGCAAGAT 1813  
Qy 2052 CTTGTGTGAGTGAAGACCTGTGAAGATGCAAGTGAATGACGACGAAAGCTTCCACCG 2111  
Db 1814 CTTGTGTGAGTGAAGACCTGTGAAGATGCAAGTGAATGACGACGAAAGCTTCCACCG 1873  
Qy 2112 TGAAGCGAGCTCCGACCAACCTCCAGCATGAGACATGTCMAAGTTCTATGAGGCTGTG 2171  
Db 1874 TGAAGCGAGCTCCGACCAACCTCCAGCATGAGACATGTCMAAGTTCTATGAGGCTGTG 1933  
Qy 2172 CGTGAAGGCGACCCCTCATCATGATGTTTGAAGTACGAAAGCATGAGGGAATTCACAA 2231  
Db 1934 CGTGAAGGCGACCCCTCATCATGATGTTTGAAGTACGAAAGCATGAGGGAATTCACAA 1993  
Qy 2232 GTTCTCTAGGGCAACGGGCTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2291  
Db 1994 GTTCTCTAGGGCAACGGGCTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2053

Qy 2292 ACTGACGAGTCGAGATGCTGTCAATATAGCCACAGATGCGCGGGCATGTCTACT 2351  
Db 2054 ACTGACGAGTCGAGATGCTGTCAATATAGCCACAGATGCGCGGGCATGTCTACT 2113  
Qy 2352 GGCCTCCAGACATTCGTGTGACCGCGATTTGGCCACAGGAATGCTGCTGTGTGGGGA 2411  
Db 2114 GGCCTCCAGACATTCGTGTGACCGCGATTTGGCCACAGGAATGCTGCTGTGTGGGGA 2173  
Qy 2412 CTTGCTGTGAAAATTCGGGGGACTTTGGGATGTCCCGGAGCTGTACAGCATGACTACTA 2471  
Db 2174 CTTGCTGTGAAAATTCGGGGGACTTTGGGATGTCCCGGAGCTGTACAGCATGACTACTA 2233  
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Qy 2592 CACCTATGGCAAAACAGCCCTGTGTACAGCTGTCAAAATGATGATGATGATGATGATGAT 2651  
Db 2354 CACCTATGGCAAAACAGCCCTGTGTGTACAGCTGTCAAAATGATGATGATGATGATGATGAT 2413  
Qy 2652 TCAAGGCGAGTCCTGTGACGACCCCGACGTCGCCCGAGAGGTATGAGCTGATGCT 2711  
Db 2414 TCAAGGCGAGTCCTGTGACGACCCCGACGTCGCCCGAGAGGTATGAGCTGATGCT 2473  
Qy 2712 GGGGTGCTGTGAGGAGAGCCCAATGAGGAAGAAATCAAGGCAATCCTACTCTCT 2771  
Db 2474 GGGGTGCTGTGAGGAGAGCCCAATGAGGAAGAAATCAAGGCAATCCTACTCTCTCT 2533  
Qy 2772 TCAGAACTGTGGCAAGGATCTCGGTCTATCTGTGACATCTGAGATCTAGGACCTTTTCC 2831  
Db 2534 TCAGAACTGTGGCAAGGATCTCGGTCTATCTGTGACATCTGAGATCTAGGACCTTTTCC 2593  
Qy 2832 CCAGACCGATCTCTCCACAGCTACTCTCTGACAGCGGCTGAGAGATGAAATCTTTTAC 2891  
Db 2594 CCAGACCGATCTCTCCACAGCTACTCTCTGACAGCGGCTGAGAGATGAAATCTTTTAC 2653  
Qy 2892 TGCCGCTGAGAGCCACAGAGCTGTCTCTCTGACAGTATTAACATCAAGACTC 2951  
Db 2654 TGCCGCTGAGAGCCACAGAGCTGTCTCTCTGACAGTATTAACATCAAGACTC 2713  
Qy 2952 CGAAGACTCTCGAGGGAAGAGGTGTACTCTTCAATCCATAGACAGATATGACTTC 3011  
Db 2714 CGAAGACTCTCGAGGGAAGAGGTGTACTCTTCAATCCATAGACAGATATGACTTC 2773  
Qy 3012 TTTTGGCATTAATCTTTCT 3071  
Db 2774 TTTTGGCATTAATCTTTCT 2833  
Qy 3072 AAAATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 3131  
Db 2834 AAAATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2893  
Qy 3132 TGAATCAATGTGCTTGTGTCTTACTATTAATCTGTGATAGACAAAGGCTTTAACAAAG 3191  
Db 2894 TGAATCAATGTGCTTGTGTCTTACTATTAATCTGTGATAGACAAAGGCTTTAACAAAG 2953  
Qy 3192 TAAATTTGTATATAGAGACATCCAGTTTGCACCAACAATCAATCAATCAATCAATCAAT 3251  
Db 2954 TAAATTTGTATATAGAGACATCCAGTTTGCACCAACAATCAATCAATCAATCAATCAAT 3013  
Qy 3252 ATTCTGTCTTGTATGTGTGATGAAAAAAGGAAAAAATAATTTCACTTAACTTTGTC 3311  
Db 3014 ATTCTGTCTTGTATGTGTGATGAAAAAAGGAAAAAATAATTTCACTTAACTTTGTC 3073  
Qy 3312 ACTTGTGTGTGACGATATGAGAGTTTCTATGATTCATCTTATTTATTTATTTAT 3371  
Db 3074 ACTTGTGTGTGACGATATGAGAGTTTCTATGATTCATCTTATTTATTTATTTAT 3133  
Qy 3372 TACTGTCTTATTTGTTTGTGATGCTTAAGCTGTGTATTAATAAGAAAA 3422

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Db      3134 TACTGTTCTTATGTTTGGATGCTTAAGCCTGTGTATTAATAAAAAA 3184

RESULT 12
AAZ88839
ID      AAZ88839 standard; DNA; 3194 BP.
XX
AC      AAZ88839;
XX
DT      30-MAY-2000 (first entry)
XX
DB      Human trkB receptor DNA.
XX
KM      trkB; human; receptor tyrosine kinase; trkB; diagnosis; neurotrophin;
KW      neurotrophic factor; db.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      114..2582
FT              /*tag= a
FT              /product= "trkB receptor"

PN      US6027927-A.
XX
PD      22-FEB-2000.
XX
PF      01-OCT-1997; 97US-00942562.
XX
PR      18-MAR-1994; 94US-00215139.
PR      05-AUG-1994; 94US-00286846.
PR      19-MAY-1995; 95US-00444597.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Uffer R, Shelton DL, Presta LG;
DR      WPI; 2000-194832/17.
XX
DR      P-PSDB; AAY51599.
XX
PT      New human trk receptors useful in the diagnosis of various human
PT      pathological conditions associated with elevated or reduced levels of
PT      neurotrophins capable of binding trkB and/or trkC.
XX
PS      Disclosure; Col 59-64; 78pp; English.
XX
CC      This invention describes a novel isolated and purified polypeptide (I),
CC      belonging to the trk family of receptor tyrosine kinases, trkB and trkC.
CC      (I) are useful in the purification of human neurotrophic factors and in
CC      the diagnosis of various human pathological conditions associated with
CC      elevated or reduced levels of neurotrophins capable of binding trkB
CC      and/or trkC. This sequence encodes the human trkB receptor described in
CC      the method of the invention
XX
SQ      Sequence 3194 BP; 824 A; 793 C; 761 G; 816 T; 0 U; 0 Other;

Query Match      85.2%; Score 3156.6; DB 3; Length 3194;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3162; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      252 AAGAGAGCCGCAAGCGAGGAGGCTCCCGCAGCGGATGAGGAGAAAGCGCGGTGCA 311
DB      14 AAGAGAGCCGCAAGCGAGGAGGAGGCTCCCGCAGCGGATGAGGAGAAAGCGCGGTGCA 73
QY      312 GCGGAGGAGAGAGGAGCTCGGCTGAGCACTGCTGCTAGGAGATGTCCTCGATTAAGGTG 371
DB      74 GCGGAGGAGAGAGGAGCTCGGCTGAGCACTGCTGCTAGGAGATGTCCTCGATTAAGGTG 133
QY      372 GCATGAGACCGGCAATGAGCGGCTCTGAGGCTTCTGCTGAGGTGATGAGCTTCTGAG 431
DB      134 GCATGAGACCGGCAATGAGCGGCTCTGAGGCTTCTGCTGAGGTGATGAGCTTCTGAG 193
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QY      432 GGGCGCTTTGCGCTGTCACGTCGCAAAATGACAGTGCCTCGGATCTGTCAGCGCA 491
DB      194 GGGCGCTTTGCGCTGTCACGTCGCAAAATGACAGTGCCTCGGATCTGTCAGCGCA 253
QY      492 CCTTCTCCATGAGATGAGCATTTTCAGGATTTGAGACCTTAAGAGTATGATCTTGAGAA 551
DB      254 CCTTCTCCATGAGATGAGCATTTTCAGGATTTGAGACCTTAAGAGTATGATCTTGAGAA 313
QY      552 CATACCGAAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAACGAGATGATGT 611
DB      314 CATACCGAAATTTTCAATGCAAAACGAAAGGTTAGAAATCATCAACGAGATGATGT 373
QY      612 TGAAGCTTATGAGGAGCTGAGAAATCGAACATTTGGAATTCGAGTTAAATTTGAGC 671
DB      374 TGAAGCTTATGAGGAGCTGAGAAATCGAACATTTGGAATTCGAGTTAAATTTGAGC 433
QY      672 TCATTAAGCATTTCTGAAAAACAGCAACCTGACGACATCATATTTTACCAGAACAACT 731
DB      434 TCATTAAGCATTTCTGAAAAACAGCAACCTGACGACATCATATTTTACCAGAACAACT 493
QY      732 GACGAGTTTGTCTAGGAAACATTTCCGTGACCTTGAATTGCTGAACTGATCCTGTGG 791
DB      494 GACGAGTTTGTCTAGGAAACATTTCCGTGACCTTGAATTGCTGAACTGATCCTGTGG 553
QY      792 CAATCCATTTAATGCTGCTCCGTGACATTAATGAGATCAAGACTCTCCAGAGGCTAAATC 851
DB      554 CAATCCATTTAATGCTGCTCCGTGACATTAATGAGATCAAGACTCTCCAGAGGCTAAATC 613
QY      852 CAGTCCAGACACTCAGGATTTTGTACTGCTGATGCTGAATGAAAGCAGAGAAATTTCCCTGAGC 911
DB      614 CAGTCCAGACACTCAGGATTTTGTACTGCTGATGCTGAATGAAAGCAGAGAAATTTCCCTGAGC 673
QY      912 AAACCTGAGATACCAATTTGTTGCTGCTGATGCAATCTGAGCAGCCTTAACCTGAC 971
DB      674 AAACCTGAGATACCAATTTGTTGCTGCTGATGCAATCTGAGCAGCAGCTTAACCTGAC 733
QY      972 TGTGAGAGAGAAAGATCTATCACTATTCCTGATGAGGAGAGATCCGGTTCCTAA 1031
DB      734 TGTGAGAGAGAAAGATCTATCACTATTCCTGATGAGGAGAGATCCGGTTCCTAA 793
QY      1032 TATGTAATGGAGATGTTGTTAATCTGATTCCTCAACATATGATGAACAAGCAGACACA 1091
DB      794 TATGTAATGGAGATGTTGTTAATCTGATTCCTCAACATATGATGAACAAGCAGACACA 853
QY      1092 GGGCTCCTTAAGGATTAATCAATTTTCATCCGATGACAGTGGAGAGAGATCTTGTGT 1151
DB      854 GGGCTCCTTAAGGATTAATCAATTTTCATCCGATGACAGTGGAGAGAGATCTTGTGT 913
QY      1152 GCGGAAATCTTGTAGAGAGAAATCAAGTCTGTCAACCTCACTGTGATTTTGACACC 1211
DB      914 GCGGAAATCTTGTAGAGAGAAATCAAGTCTGTCAACCTCACTGTGATTTTGACACC 973
QY      1212 AACTATCACATTTCTGGAATCTCCAACTGACAGCAACCACTGATGATTCATTTCACTGT 1271
DB      974 AACTATCACATTTCTGGAATCTCCAACTGACAGCAACCACTGATGATTCATTTCACTGT 1033
QY      1272 GAAAGGCAACCCCAACCAAGCGCTTCAATGTTCTATTAACGGGCAATATGATGATGTC 1331
DB      1034 GAAAGGCAACCCCAACCAAGCGCTTCAATGTTCTATTAACGGGCAATATGATGATGTC 1093
QY      1332 CAATATCATTTGTACTTAATAATATGATTTACATGATCAACGAGATCAACGAGCTGCTCCA 1391
DB      1094 CAATATCATTTGTACTTAATAATATGATTTACATGATCAACGAGATCAACGAGCTGCTCCA 1153
QY      1392 GCTGGAATATCCACTCACATGAACATGAGGAGCTCACTCTAATAGCCAAAGATGAGTA 1451
DB      1154 GCTGGAATATCCACTCACATGAACATGAGGAGCTCACTCTAATAGCCAAAGATGAGTA 1213
QY      1452 TGGGAAAGATGAGAAACAGATTTTCTGCTCACTTATGAGGCTGAGCTGGAATGAGATGAG 1511
DB      1214 TGGGAAAGATGAGAAACAGATTTTCTGCTCACTTATGAGGCTGAGCTGGAATGAGATGAG 1273
QY      1512 TGCAAACCCAAATTAATCTGATGATTAATTAATGAAGATTAAGAACTGACAGCAATGACAT 1571
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Db      1274  TCGAAACCAATTATCTGTATGTATATGAAATATGAACTGACAGGAATGACAT 1333
Oy      1572  CGGGGACACCAAGACAGAAATGAAATCCCTTCCACAGACGTCATGATTAACCGG 1631
Db      1334  CGGGGACACCAAGACAGAAATGAAATCCCTTCCACAGACGTCATGATTAACCGG 1393
Oy      1632  TCGGGAACATCTCTCGCTCTATGCTGTGTGTGATTCGCTGTGTGTGGATTTTGCT 1691
Db      1394  TCGGGAACATCTCTCGCTCTATGCTGTGTGTGATTCGCTGTGTGTGGATTTTGCT 1453
Oy      1692  TTTGGTAATGCTGTTTCTGCTTAAGTTGGCAAGACATCCAAAGTTGGCATGAAAGCCC 1751
Db      1454  TTTGGTAATGCTGTTTCTGCTTAAGTTGGCAAGACATCCAAAGTTGGCATGAAAGCCC 1513
Oy      1752  AGCCCTCGTTATCAGCAATGATGATGATCTGCGCCGCCATCCCATCACTCTCCAAATGG 1811
Db      1514  AGCCCTCGTTATCAGCAATGATGATGATCTGCGCCGCCATCCCATCACTCTCCAAATGG 1573
Oy      1812  GAGTAAACATCTCATCTTCTGCGAAGTGGCCAGATGCTGTCATTATTTGGAATGACCA 1871
Db      1574  GAGTAAACATCTCATCTTCTGCGAAGTGGCCAGATGCTGTCATTATTTGGAATGACCA 1633
Oy      1872  GATCCCTGTCAATTGAAAAATCCCAAGTACTTTGGCAATCAACAGTCACTCAAGCCAGA 1931
Db      1634  GATCCCTGTCAATTGAAAAATCCCAAGTACTTTGGCAATCAACAGTCACTCAAGCCAGA 1693
Oy      1932  CACATTTGTTGACGACATCAACAGCAATTAATTTGTTGAAAAAGGAGCTAGGGAAGG 1991
Db      1694  CACATTTGTTGACGACATCAACAGCAATTAATTTGTTGAAAAAGGAGCTAGGGAAGG 1753
Oy      1992  AGCCCTTGGAAAAAGTGTCTAGCTGAAATGCTATAACCTGTCTGAGCAGGACAAAGT 2051
Db      1754  AGCCCTTGGAAAAAGTGTCTAGCTGAAATGCTATAACCTGTCTGAGCAGGACAAAGT 1813
Oy      2052  CTTGTGTGACATGAAAGACCTCTGAAAGATGCGCAGTACATGACGCAAGGACTTTCACCG 2111
Db      1814  CTTGTGTGACATGAAAGACCTCTGAAAGATGCGCAGTACATGACGCAAGGACTTTCACCG 1873
Oy      2112  TGAGGCCAGACTCTGACCAACCTCCAGATGACACATGCTCAAGTTCTATGGGCTCTG 2171
Db      1874  TGAGGCCAGACTCTGACCAACCTCCAGATGACACATGCTCAAGTTCTATGGGCTCTG 1933
Oy      2172  CGTGAAGGCGACCCCTCATATGCTCTTGAAGTACATGAAAGCATGGGGAATCTCAACA 2231
Db      1934  CGTGAAGGCGACCCCTCATATGCTCTTGAAGTACATGAAAGCATGGGGAATCTCAACA 1993
Oy      2232  GTTCTCAGGGGACACGCGCTGATGCGGTGCTGATGCGTGAAGGCAACCCGCCACGGA 2291
Db      1994  GTTCTCAGGGGACACGCGCTGATGCGGTGCTGATGCGTGAAGGCAACCCGCCACGGA 2053
Oy      2292  ACTGAACGAGTGCAGATGCTGATATAGCCAGAGATGCGCGCGGATGCTTACT 2351
Db      2054  ACTGAACGAGTGCAGATGCTGATATAGCCAGAGATGCGCGCGGATGCTTACT 2113
Oy      2352  GGCCTCCACGACCTTCTGACACCGGATTTGGCCACAGGAACTGCTGTGTGGGGAGAA 2411
Db      2114  GGCCTCCACGACCTTCTGACACCGGATTTGGCCACAGGAACTGCTGTGTGGGGAGAA 2173
Oy      2412  CTTGCTGGAATAATCGGGGACTTTGGGATGTCGGGGGACGTGTAACAGCACTGACTACTA 2471
Db      2174  CTTGCTGGAATAATCGGGGACTTTGGGATGTCGGGGGACGTGTAACAGCACTGACTACTA 2233
Oy      2472  CAGGGTCGGTGGCCACACAAATGCTGCCATTCGCTGATGCTCTCAGAGAGCATATGTA 2531
Db      2234  CAGGGTCGGTGGCCACACAAATGCTGCCATTCGCTGATGCTCTCAGAGAGCATATGTA 2293
Oy      2532  CAGGAAATTCAGACAGGAAAGGAGCTGTGAGGCTGTGGGGGTCTGTTTGTGGGAATTT 2591
Db      2294  CAGGAAATTCAGACAGGAAAGGAGCTGTGAGGCTGTGGGGGTCTGTTTGTGGGAATTT 2353
Oy      2592  CACCTATGCAAAACAGCCTGTGTAACAGCTGTCAAAACATGAGTGATAGATGATCAC 2651

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Db      2354  CACCTATGCAAAACAGCCTGTGTATCAAGCTGTCAAAACATAGAGTGATAGAGTATCAC 2413
Oy      2652  TCAAGGCCAGTCTGTGACGACCCCGCAGCTGCCCCAGAGGTGTATGATGATGCT 2711
Db      2414  TCAAGGCCAGTCTGTGACGACCCCGCAGCTGCCCCAGAGGTGTATGATGATGCT 2473
Oy      2712  GGGGTGCTGACGAGAGAGCCCATATGAGAGAAACATCAAGGCAATCCATACCTCT 2771
Db      2474  GGGGTGCTGACGAGAGAGCCCATATGAGAGAAACATCAAGGCAATCCATACCTCT 2533
Oy      2772  TCAAACTGGCCAAAGGATCTCGGTCTACCTGGAACATTCCTAGGCTAGGGCCCTTTCC 2831
Db      2534  TCAAACTGGCCAAAGGATCTCGGTCTACCTGGAACATTCCTAGGCTAGGGCCCTTTCC 2593
Oy      2832  CCAGACCGATCTCTCCCAAGCTACTCTCAGACGGGCTGAGAGATGAAACATCTTTTAC 2891
Db      2594  CCAGACCGATCTCTCCCAAGCTACTCTCAGACGGGCTGAGAGATGAAACATCTTTTAC 2653
Oy      2892  TGCCGCTGAGGACCAACAGCTGCTCTTCACTGTGACAGTATTAATCAAGACTC 2951
Db      2654  TGCCGCTGAGGACCAACAGCTGCTCTTCACTGTGACAGTATTAATCAAGACTC 2713
Oy      2952  CGAAGACTCTCGAGGAGAGAGTGTATCTTCTCACTCAATGACACAGATTAAGACTTC 3011
Db      2714  CGAAGACTCTCGAGGAGAGAGTGTATCTTCTCACTCAATGACACAGATTAAGACTTC 2773
Oy      3012  TTTTGGATTAATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3071
Db      2774  TTTTGGATTAATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2833
Oy      3072  AAATTTCTTTTCTCTCTTTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3131
Db      2834  AAATTTCTTTTCTCTCTTTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2893
Oy      3132  TGAATCAATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3191
Db      2894  TGAATCAATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2953
Oy      3192  TAAATTTGTTATAGACGACACAGTTCAGTTGGCCACACAACTAACAAATGCTGTGT 3251
Db      2954  TAAATTTGTTATAGACGACACAGTTCAGTTGGCCACACAACTAACAAATGCTGTGT 3013
Oy      3252  ATTCTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3311
Db      3014  ATTCTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3073
Oy      3312  ACTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3371
Db      3074  ACTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3133
Oy      3372  TACTGTTCTTATGTTTGTGATGCTTAAGCTGTGTATTAAGGAAAA 3422
Db      3134  TACTGTTCTTATGTTTGTGATGCTTAAGCTGTGTATTAAGGAAAA 3184

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## RESULT 13

AAT51457 standard; DNA; 3060 BP.

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ID      AAT51457
XX      AAT51457;
AC      16-OCT-2003 (revised)
DT      27-AUG-2003 (revised)
DT      30-APR-1997 (first entry)
DE      gd,lrkb fusion useful in kinase receptor activation assay.
XX      kinase receptor activation; KIRA; receptor protein tyrosine kinase; rPTK;
XX      signal transduction; autophosphorylation; gd,lrkb;
XX      enzyme-linked immunosorbent assay; ELISA; de.
OS      Human herpesvirus 1.
OS      Homo sapiens.

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OS Chimeric.
XX
FH Key Location/Qualifiers
FT misc_RNA 4
FT /*tag= a
FT /note= "sp6 RNA start"
FT misc_RNA 79
FT /*tag= b
FT /note= "begin gd from pchadIII"
FT CDS 307..2850
FT /*tag= c
FT /product= "gd.trkB fusion protein"
FT sig_peptide 394..484
FT /*tag= d
FT /note= "trkB signal sequence"
FT mat_peptide 485..2847
FT /*tag= e
FT /note= "mature trkB"
FT polyA_signal 3023
FT /*tag= f
FT /note= "SV40 early polyA"
XX
PN MO9514930-A1.
XX
PD 01-JUN-1995.
XX
PF 18-NOV-1994; 94MO-US013329.
XX
PR 23-NOV-1993; 93US-00157563.
PR 20-DEC-1993; 93US-00170558.
PR 05-AUG-1994; 94US-00286305.
XX
PA (GETH ) GENENTECH INC.
XX
PI Godowski PJ, Mark MR, Sadiq MD, Wong WLT;
XX
DR WPI: 1995-207042/27.
DR P-PSDB; AAM11941.
XX
PT Measuring auto-phosphorylation of tyrosine kinase receptor - to identify
PT and characterise potential (ant)agonists of TKR.
XX
PS Example 3; Fig 13a-g; 148bp; English.
XX
CC DNA constructs (AAT51456-58) respectively code for gd.trkA (AAM11940),
CC gd.trkB (AAM11941) and gd.trkC (AAM11942), comprising fusions between
CC herpes simplex virus glycoprotein D flag polypeptide and human receptor
CC protein tyrosine kinases (trPKs) trkA, B and C, which are involved in the
CC interaction between neurotrophins and their target cells. The gd.trk
CC constructs can be expressed e.g. in dp12.CHO host cells and used in
CC kinase receptor activation, enzyme-linked immunosorbent assays (ELISA
CC ELISA) to measure autophosphorylation of trPK kinase domains. These
CC assays are used to identify and characterise potential (ant)agonists of
CC trPKs, study ligand-receptor interactions, measure phosphatase activity
CC and identify trPK ligands in clinical samples. (Updated on 27-AUG-2003 to
CC correct OS field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 3060 BP; 782 A; 804 C; 744 G; 730 T; 0 U; 0 Other;
Query March 67.9%; Score 2516.2; DB 2; Length 3060;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2518; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 445 TGTCCACGCTCTGCAAAATGACAGTGCCTCTGAGATCTGTGTCAGAGACCTTCTCTGGC 504
Dd 475 TGTCCACGCTCTGCAAAATGACAGTGCCTCTGAGATCTGTGTCAGAGACCTTCTCTGGC 534
QY 505 ATGTGCGATTTCGAGATTGAGAGCTTAACAGTGTAGATCTCTGAGAACATCACCGAAATT 564
Dd 535 ATGTGCGATTTCGAGATTGAGAGCTTAACAGTGTAGATCTCTGAGAACATCACCGAAATT 594
QY 565 TTTCATCGAAACGAGAAAGGTTAGAAATCATCAACGAAAGTATGTTGAAGCTTAATGTG 624
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Dd 595 TTTCATCGAAACGAGAAAGGTTAGAAATCATCAACGAAAGTATGTTGAAGCTTAATGTG 654
QY 625 GAGCTGAGAAATCTGACAAATGTGGAATCTGGAATTAAATTTGTGCTCATTAAGCATTT 684
Dd 655 GAGCTGAGAAATCTGACAAATGTGGAATCTGGAATTAAATTTGTGCTCATTAAGCATTT 714
QY 685 CTGAAAAACGAGAACCTGAGCAGCATCAATTTTACCAGAAACAAATCGAAGTTGTCT 744
Dd 715 CTGAAAAACGAGAACCTGAGCAGCATCAATTTTACCAGAAACAAATCGAAGTTGTCT 774
QY 745 AGGAAACATTTCCGTCACCTTGACCTTGTCTGAACCTGATCTCTGATGAGCAATTCATTA 804
Dd 775 AGGAAACATTTCCGTCACCTTGACCTTGTCTGAACCTGATCTCTGATGAGCAATTCATTA 834
QY 805 TGCTCTGTGACATTAATGTGATGAACTCTCCAGAGGCTTAATCACTCAAGACACT 864
Dd 835 TGCTCTGTGACATTAATGTGATGAACTCTCCAGAGGCTTAATCACTCAAGACACT 894
QY 865 CAGGATTTGTAACCTGCGTGAATGAAAGCAGAAAGAAATTTCCCTGGCAACCTGCAGATA 924
Dd 895 CAGGATTTGTAACCTGCGTGAATGAAAGCAGAAAGAAATTTCCCTGGCAACCTGCAGATA 954
QY 925 CCCAATTGTGTTTGGCATCTGCAAAATCTGAGCGACCTTAACCTCACTGTGAGAGAGAGA 984
Dd 955 CCCAATTGTGTTTGGCATCTGCAAAATCTGAGCGACCTTAACCTCACTGTGAGAGAGAGA 1014
QY 985 AAGTCTATCACTTATCTCTGATGTGAGCAGTGTATCCGGTCTTAATATGATTTGGAT 1044
Dd 1015 AAGTCTATCACTTATCTCTGATGTGAGCAGTGTATCCGGTCTTAATATGATTTGGAT 1074
QY 1045 GTTGTGTAACCTGTTTCCAAACAATGAAATGAAACCAAGCCACACAGGCTCTTAAGG 1104
Dd 1075 GTTGTGTAACCTGTTTCCAAACAATGAAATGAAACCAAGCCACACAGGCTCTTAAGG 1134
QY 1105 ATAACTTAACATTTATCTCCGATGACAGTGGGAAACAGATCTCTGTGTGCGGAAAAATCTT 1164
Dd 1135 ATAACTTAACATTTATCTCCGATGACAGTGGGAAACAGATCTCTGTGTGCGGAAAAATCTT 1194
QY 1165 GTAAGAGAGATCAAGATTTCTGTCAACCTGATGTGATTTTGCAACCAATATCAATTT 1224
Dd 1195 GTAAGAGAGATCAAGATTTCTGTCAACCTGATGTGATTTTGCAACCAATATCAATTT 1254
QY 1225 CTGGAATCTTCCAACTCTGACACACAGCTGTGATTCATTTCACTGTGAAAGGCAACCC 1284
Dd 1255 CTGGAATCTTCCAACTCTGACACACAGCTGTGATTCATTTCACTGTGAAAGGCAACCC 1314
QY 1285 AAACAGCGCTTCAAGTGTCTTAATTAACGGGCAATATGAAATGATCCAAATCATCTGT 1344
Dd 1315 AAACAGCGCTTCAAGTGTCTTAATTAACGGGCAATATGAAATGATCCAAATCATCTGT 1374
QY 1345 ACTAAATACATGTATACCAATCAACAGAGTACACAGGCTGCTCCAGCTGATTAATCCC 1404
Dd 1375 ACTAAATACATGTATACCAATCAACAGAGTACACAGGCTGCTCCAGCTGATTAATCCC 1434
QY 1405 ACTCACTGAACCAATGGGAGCTACCTTAATGACCAGAAATGATATGGAAGATGAG 1464
Dd 1435 ACTCACTGAACCAATGGGAGCTACCTTAATGACCAGAAATGATATGGAAGATGAG 1494
QY 1465 AAACAGATTTCTGTCACCTTCAAGGCTGAGCTGGAATTTGACGATGTAACCCCAAT 1524
Dd 1495 AAACAGATTTCTGTCACCTTCAAGGCTGAGCTGGAATTTGACGATGTAACCCCAAT 1554
QY 1525 TATCTGATGTAAATTTATGAAGATTAATGAACTGACAGCGAATGACATCGGAGACACCA 1584
Dd 1555 TATCTGATGTAAATTTATGAAGATTAATGAACTGACAGCGAATGACATCGGAGACACCA 1614
QY 1585 AACAGAAATATGAATCCCTTCCACAGAGCTCACTGATTAACCCGCTGGGAAACATCTC 1644
Dd 1615 AACAGAAATATGAATCCCTTCCACAGAGCTCACTGATTAACCCGCTGGGAAACATCTC 1674
QY 1645 TCGGTCTAGTGTGATGATGATTTGCGGTCTGTGTGATGATTTTGGCTTTGATATGCTG 1704
Dd 1675 TCGGTCTAGTGTGATGATGATTTGCGGTCTGTGTGATGATTTTGGCTTTGATATGCTG 1734
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QY 1705 TTTCGTAAAGTGGCAAGACCTCCAAAGTTTGGCATGAAAGGCCAGCCTCCGTTATC 1764
D 1735 TTTCGTAAAGTGGCAAGACCTCCAAAGTTTGGCATGAAAGGCCAGCCTCCGTTATC 1794
QY 1765 AGCAATATGATGATCTGCCAGGCCCTCCATCACTTCCAAATGGAGTAACTCA 1824
D 1795 AGCAATATGATGATCTGCCAGGCCCTCCATCACTTCCAAATGGAGTAACTCA 1854
QY 1825 TCTTCTTGGAAAGGTGGCCAGATGCTGTCAATTATGGAATGACCAAGATCCCGTCA 1884
D 1855 TCTTCTTGGAAAGGTGGCCAGATGCTGTCAATTATGGAATGACCAAGATCCCGTCA 1914
QY 1885 GAAATCCCGAGTACTTTGGCATCAACAGAGCTCAAGCAGACACTTTGTCAG 1944
D 1915 GAAATCCCGAGTACTTTGGCATCAACAGAGCTCAAGCAGACACTTTGTCAG 1974
QY 1945 CACATCAAGGACATTAACATTTGTTCTGAAAAGGAGCTAGGCGAAGAGCTTTG 2004
D 1975 CACATCAAGGACATTAACATTTGTTCTGAAAAGGAGCTAGGCGAAGAGCTTTG 2034
QY 2005 GTGTTCTAGCTGAATGCTAATACCTGCTCTGAGAGGACAAAGATCTTGTTGGCAG 2064
D 2035 GTGTTCTAGCTGAATGCTAATACCTGCTCTGAGAGGACAAAGATCTTGTTGGCAG 2094
QY 2065 AAGACCTGAAGGATGCGCAGTGAATGACAGCAAGACTTCCACCGTGAAGGCCAG 2124
D 2095 AAGACCTGAAGGATGCGCAGTGAATGACAGCAAGACTTCCACCGTGAAGGCCAG 2154
QY 2125 CTGACCAACCTCCAGCATGAGACATCGTCAGATTCTATGCGCTGTCGTGAGAGG 2184
D 2155 CTGACCAACCTCCAGCATGAGACATCGTCAGATTCTATGCGCTGTCGTGAGAGG 2214
QY 2185 CCCCCTCATGATGCTTTGAGTACATGAAAGATGGGGAACCTCAAGATTCTCAAG 2244
D 2215 CCCCCTCATGATGCTTTGAGTACATGAAAGATGGGGAACCTCAAGATTCTCAAG 2274
QY 2245 CACGCGCCTGATGCGCTGATGATGCTGAGGGGCAACCGCCACAGGAACTGAG 2304
D 2275 CACGCGCCTGATGCGCTGATGATGCTGAGGGGCAACCGCCACAGGAACTGAG 2334
QY 2305 CAGATGCTGATATAGCCCAAGACATGCGCGGGGCAATGCTCTGCTGCTCCAC 2364
D 2335 CAGATGCTGATATAGCCCAAGACATGCGCGGGGCAATGCTCTGCTGCTCCAC 2394
QY 2365 TTGCTGACCGCCATTTGGGCGACAGAACTGCTGCTGCGGGGAACTTGCTG 2424
D 2395 TTGCTGACCGCCATTTGGGCGACAGAACTGCTGCTGCGGGGAACTTGCTG 2454
QY 2425 ATCGGGGACTTTGGGATGTCGCCGGAGCTGTACAGCACTGACTCAAGGGTGG 2484
D 2455 ATCGGGGACTTTGGGATGTCGCCGGAGCTGTACAGCACTGACTCAAGGGTGG 2514
QY 2485 CACAAATGCTGCCATTTGCTGATGCTTCCAGAGACATCATGACAGAAATTAC 2544
D 2515 CACAAATGCTGCCATTTGCTGATGCTTCCAGAGACATCATGACAGAAATTAC 2574
QY 2545 ACGGAAAGCGAGCTGTGAGCTTGGGGTCTGTTTGGGAGATTTTCACTTATG 2604
D 2575 ACGGAAAGCGAGCTGTGAGCTTGGGGTCTGTTTGGGAGATTTTCACTTATG 2634
QY 2605 CAGCCCTGATACCAAGCTGTCAAATGAGGTGATAGAGTATCACTCAGGGCCG 2664
D 2635 CAGCCCTGATACCAAGCTGTCAAATGAGGTGATAGAGTATCACTCAGGGCCG 2694
QY 2665 CTGAGAGGACCCCGCAGTGGCCCGCAGAGGCTGTATGAGCTGATGCTGGG 2724
D 2695 CTGAGAGGACCCCGCAGTGGCCCGCAGAGGCTGTATGAGCTGATGCTGGG 2754
QY 2725 CGAGAGCCCACTGAGAGAGAACTCAAGGGCACTCAATCCTTCCAGACTTGG 2784
D 2755 CGAGAGCCCACTGAGAGAGAACTCAAGGGCACTCAATCCTTCCAGACTTGG 2814
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QY 2785 AAGGCACTCCCGGTCTAAGTGAATTTAGGCTAGAGGCGCTTTTCCCAAGACGAT 2844
D 2815 AAGGCACTCCCGGTCTAAGTGAATTTAGGCTAGAGGCGCTTTTCCCAAGACGAT 2874
QY 2845 TCCCAAGTACTCTCTGAGAGGGGCTGAGAGATGAATCTTTTAACTTCCGCTGAG 2904
D 2875 TCCCAAGTACTCTCTGAGAGGGGCTGAGAGATGAATCTTTTAACTTCCGCTGAG 2934
QY 2905 CACCAAGCTGCTCTCTTCACTGACATTAATTAACATCAAGACTCCGAGAACTCT 2964
D 2935 CACCAAGCTGCTCTCTTCACTGACATTAATTAACATCAAGACTCCGAGAACTCT 2994
QY 2965 A 2965
D 2995 A 2995

RESULT 14
ADB79772
ID ADB79772 standard; DNA; 4757 BP.
XX
AC ADB79772;
XX
DT 04-DEC-2003 (first entry)
XX
DE Rat neural receptor protein-tyrosine kinase, trkB, DNA, SEQ ID 12.
XX
KW Analgesic; pain; streptozocin-induced diabetes; rat; gene; ds.
XX
OS Rattus norvegicus.
XX
PN BP1279744-A2.
XX
XX 29-JAN-2003.
XX
PE 26-JUL-2002; 2002EP-00255249.
XX
PR 27-JUL-2001; 2001GB-00018354.
PR 07-FEB-2002; 2002GB-00002910.
XX
PA (WARN) WARNER LAMBERT CO.
PI Brookbank RA, Dixon AK, Lee K, Pimock RD;
XX
DR WPI: 2003-395407/38.
XX
P-PSDB; ADB79771.
XX
PT Use of isolated gene sequences and encoded polypeptides that are
PT upregulated in the spinal cord in response to streptozocin-induced
PT diabetes for screening compounds for the treatment of pain, or for
PT diagnosing pain.
XX
PS Claim 1; Page 57-58; 334pp; English.
XX
CC The present invention relates to nucleotide sequences which are useful in
CC the screening of compounds for the treatment of pain, or for the
CC diagnosis of pain. The nucleotide sequences are up-regulated in the
CC spinal cord in response to streptozocin-induced diabetes. The present
CC sequence is one such nucleotide sequence.
XX
SQ Sequence 4757 BP; 1122 A; 1288 C; 1197 G; 1150 T; 0 U; 0 Other;

Query Match 61.1%; Score 2264.2; DB 10; Length 4757;
Best Local Similarity 79.5%; Pred. No. 0;
Matches 2919; Conservative 0; Mismatches 618; Indels 134; Gaps 15;

QY 74 GGGCCATGACGACGCGCGCGCGGAGCTCCGAGACGCGGTAGCGCCCGCTTAAGC 133
D 390 GAGCCACCGAGTGGCGCTGCGCTATGACACATGACGCGCGCTTGCGCTTGAAGAC 449
QY 134 GTTTCGTATGCGGGGACCACTGAACTTGGCGCTTGGCGGAACTCTTGGCTC--- 190
D 450 GGGCGGATGTTCCAGCCACTGTAACCATTTGGTCAAGGCGCAACTGCTCAGCCCG 509
```



OY	191	--CGAGCAAGCTCAGGCTCTGTATAGTCTGAGACTGCGCACGCGCCGACACAGACCCAGAGA	248
Db	510	CACCGACAGGGCTCAGGCTCTGTGTACGCTCTCTCGCGCGGAGGCGATCAGACAC-----	563
OY	249	GTTTAAGAGAGCGCGAAGCGCACAGGAGAGGAGCTCCCGCACAGGAGTGGGAGAAAGCGGCGGT	308
Db	564	---AAGCAGCAGAAGAGGCTCAGGGAGAGGAGCTCCCGCTCCGCGGGGGA---CGCTGGC	617
OY	309	CGAGCGCGGAGACAGGCACTCGGG---CTGGCACTGGCTGTAGGGATGTCGTCCTGGA	364
Db	618	TCAGGTGTGGGACACGCACTGTGACTGTGCACTGGCACTGGCACTCGGAGATGTGCGCTCGGC	677
OY	365	TAAAGTGGACATGGAGCCGCGCANAGCGGAGGCTCTGGGAGCTTCTGGCTGGCTGGTGTGGGCT	424
Db	678	CGAGGTGGCATGGAGCCCGCATGGCGCGGACTCTGGGAGCTTATGCTGTGGATCTTGGGCT	737
OY	425	TCGGAGGGGCGGCTTTCGCTGTGCCAGTCTGTGCAATGGCAGTCCCTCGGATCTGGT	484
Db	738	TCGGAGGGGCTTCTCTTCCTGTGCCCACTGTCTGGAAATGGACACCACTAGATTTGGT	797
OY	485	GCAAGGACCCCTTCCTCCCTGGCATCGTGGGATTTCCGAGTTGGAGCCTTAACGTGTATATC	544
Db	798	GTACCGAGCCCTTCTCTGGCATCTGGGATTTCCAGGATGTGAACCTTAACGACATGTACC	857
OY	545	CTGAGAACATCAACCCAAATTTTTCATCTGCAAAACAGAAAAGGTTAGAAATCATCAACGAG	604
Db	858	CAGAGAACATCAACCGAAATTTCTCANTGGCAACAGAAAAGGTTAGAAATCATCATAGAG	917
OY	605	ATGATGTTGAAAGCTTATGTGGAGCTGAGAAATCTGCACAATTGTGGATTCTGGATTAATAT	664
Db	918	ATGATGTTGAAAGCTTACGTGGGAGCTGAAAACCTTTCACATTTGTGGATTCCGGCTTAAAGT	977
OY	665	TTGTGGCTCATPAAGCATTTCTGAAAACACAGAACCTGACACATCAATTTTACCCGAA	724
Db	978	TTGTGGCTTTCACAGGCGTTTCTGAAAGAACGGCAACCTGGGCAATCAATTTCACTGGA	1037
OY	725	ACAAACTGACGAGTTTGTCTAGAAACATTTCCGTACCTTGACTGTCTGAACTGATCC	784
Db	1038	ACAAAGCTACGAGTTTGTCCAGGAACATTTCCGCACTTGACTGTGACCTGATCC	1097
OY	785	TGTGGGGCAATCCATTTCATGCTCCCTGTGCATTAATGTGGATCAAGACTCTCCAAAGG	844
Db	1098	TGACGGGTAAATCCGTTCACGTGTCTGTGACATCATGTGGCTCAAGACTCTCCAGAGA	1157
OY	845	CTAAATCCAGTCCAGACACTCAGATTTGTACTGCTGATAGAAAGCAGCAAGATATTC	904
Db	1158	CGAATTCAGGCCCGACACTCAGATTTGTATGTGCTCAATGAGAGCAGCAAGATATCC	1217
OY	905	CCCTGGCAAACTGTGAGTACCCTAATTTGTGTTTGCCATCTGCAAAATTTGGCCCGACCTA	964
Db	1218	CTGTGGCAAACTGTGAGTATCCCAATTTGTGTCTGCGCTGTGCACTGTGCGCTGCTCTA	1277
OY	965	ACCTCACTGTGGAGAGAGAAAGTCTATACATTAATCCGTATAGTGTGGCAGGTGATCCGG	1024
Db	1278	ACCTCAAGGTGGAGAGAGAGAGTCTGTGACCATTTCTGTGACGCTCGGGGATGACCTGC	1337
OY	1025	TTCTAATATATGATTGGGATGTTGGTAACTGTGTTTCCAAATATATGAAATGAACAAGCC	1084
Db	1338	TTCCCAACTTGTATCTGGGACGTTGGGAATTTGGTTTCCAAACATGATGAACAAAGCC	1397
OY	1085	ACACACAGGGCTCTTAAGAGTAACTTAATTTTCATCCGATGACAGTGTGGAGACAGATCT	1144
Db	1398	ACACACAGGGCTCTTAAGAGTAAACCAATTTTCATCGAGTACAGTGTGGAAACCAATCT	1457
OY	1145	CTTGTGTGGCGGAAATCTGTGAGAGAGATCAAGATTTCTGTCAACTGTGACCTGACATY	1204
Db	1458	CTTGTGTGGCAGAAAACCTCGTGGAGAGATCAAGACTCTGTGAACCTCACTGTGACATY	1517
OY	1205	TTGACCAACTATCAATTTCTGAACTTCCAACTTGACCACTGATGATTCAT	1264
Db	1518	TTGACCAACTATCAATTTCTGAACTTCCAACTTGACCACTGATGATTCAT	1577

[illegible]



Db	2655	TTTACTCTGGCATCCCAACATTTCTGGTACCCAGACTCTGGCCACCCCGAGACTGCTTGGTAG	2714
Oy	2405	GGAGAACTTGCTGGTGAATAATCGGGACCTTTGGAGATGTCCCGGACGTGTACACACTG	2464
Db	2715	GAGAGAACTCTGGTGAATAATTTGGGGACCTTCGGGATGTCTCCCGGATGTATACAGACCG	2774
Oy	2465	ACTACTACAGGGTGGGTGGCCACACATATGCTGCCATTTCGTGTGATGCTTCCAGAGACA	2524
Db	2775	ACTACTACCGGGTGGTGGCCACCAATGTTGCCATCCGATGTGATGCTTCCAGAGACA	2834
Oy	2525	TCATGTACAGAAATTTCAACAACGAGATGACGTCTGAGCTGGGGGCTCGTTGTGGG	2584
Db	2835	TCATGTACAGAAATTTCAACAACGAGATGACGTCTGAGCTGGGAGTTGTGTGGG	2894
Oy	2585	AGATTTTACCTATGCAACAGAGCCCTGTACCAAGCTGTCAACATGAGGTGATAGAT	2644
Db	2895	AGATTTTACCTATGCAACAGAGAGCCCTGTATACGCTATCAACATCAAGGTGATAGAT	2954
Oy	2645	GTATACACTCAGGGCCGAGTCTGTACAGCACCCCGCAGCTGCCCGGAGGTTATGAC	2704
Db	2955	GCATCACCCCAAGGGCAGATCCTTCAAGCGGCTCGACCTGTCTCCAGAGGTTATACGAC	3014
Oy	2705	TGATGCTGGGGTGCTGGAGGAGAGAGCCCCACATGAGGAATAACAATCAAGGGCATCCATA	2764
Db	3015	TGATGCTGGGATGCTGGAGGAGGAGACACACACAAAGGAATAACATCAAGAACTACACA	3074
Oy	2765	CCCTCTCTCAAACTTGGCCAAAGGATCTCGGTACTCTGAGACATTTAGAGCTAG--GGC	2823
Db	3075	CACCTCTTCAAACTTGGCGAAAGGAGTGGCCGCTACTGTACTGTACATCTTACGTTAGACTC	3134
Oy	2824	CCTTTTCCTCCAGACCGATCTTCCCAACGTATCTCTCAAGCGGCTGAGAGATGAAAT	2883
Db	3135	CCTCTCTCCAGAGGCGCTTCTCCAAAGCACCTCTCAGAC-----	3175
Oy	2884	CTTTTAATGCGCGTGGAGGCCACCAACCTCTCTCTTCACTCGAATATTAATATATC	2943
Db	3176	CTTTTAATGCGCGCT--GATGTACACACTTGTGTCTTGTGCTGTGAAGTGTAAACA--	3222
Oy	2944	AAAGACTCCGAAAGCTCTCGAGGGAAACAGTGTATCTTCTTCACTATAGACACAGTA	3003
Db	3233	AGACAGAGAGCGGCTCTCCGGGTGAGGACATGGGCACTTCCCATTCACAG--ACAGTA	3299
Oy	3004	TTGACTTCTTTTGGCATTATCTCTTCTCTC-----	3035
Db	3291	TCGACTCGCTCTGGCTTTGTGTGCTTCTCTCCCTTGGTGTGTTCTTCTTTTGTGdCA	3350
Oy	3036	-----TTTCATCTCCCTTGGTGTCTTCTTCTT	3067
Db	3351	TTCTCCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT	3410
Oy	3068	TTTTAAATTTCTTTTCTCTTTTCTTTTGTGCTTCCGTGCTACGATCTTACCCCTT	3127
Db	3411	CTATCTATCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT	3470
Oy	3128	CTTTTGAATCAATCGGCTCTGCACTTATTAATCTGTGATAGACAAAGGCTTTAAACA	3187
Db	3471	CTCTGTGACGATCTGGCTCTGTGATCTCTATTCATCTATAGACAAAGGCTTTAAACA	3530
Oy	3188	AACTGAATTTGTTATATCAGACAGACATTCAGTTTGCACACAACTAACAGATGCTTGG	3247
Db	3531	AACTGAATTTGTTATATCAGACAGACATTCAGTTTGCACACAACTAACATGCTTGG	3590
Oy	3248	TTGATTCCTGCTTGAATGTGAGTGAAGAAAAAGGAAAAACAATAT-----TCACTT	3301
Db	3531	TTGATTCCTGCTTGAATGTGAGTGAAGAAAAAGGAAAAACAATATCAAACTTCAAC	3650
Oy	3302	AAACTTGTCACTTCTGCTGTACAGATATCGAGATTTCTATGTGATTCATCTTATTTAT	3361
Db	3651	TTAAACGTCACCTTCCGATGTACACACAGGGGCGTTTCTATGTGATTCATCTTATTTAT	3710
Oy	3362	TTAT-----TATTTATCTGTCTTATTTGTTTTTGTGATGCTTAAAG	3402

Db	3712	CTATTTAATTATATCATTTATTTATTTCTCTCTTTGGTTTCCG9TGGTTTAG	3770
Qy	3403	CCGTGTGATATAAAAAAGAAACCTGTGTTCATCTGTGAGACCTTTATCTATGGAGATT	3462
Db	3771	CCCTGTGTATGAGAAAGGAAAGTCATGTATCACTGTGGAAAACTTTATCTGTGGAAAAATGG	3830
Qy	3463	AAACCAG--GAGAGAAGATTATATATGACCGCAATATGGAGGAAACAAAGACAAC	3520
Db	3831	AAACCAGAGGGGAAAGAGAGCTTTACATTAAGACAGCAGAGATGAGACACAGAAAAGC	3890
Qy	3521	ACTGGGATACAGCTGTGTCTAGTCCCTACTTAAAGAAATATCAGCAACTGTGTAGCTGGAA	3580
Db	3891	CATTCGATTCAGCCAGAGATCGCTCTGTGAT--AGGAAAACCGACAGCATTCAGCTGGAG	3948
Qy	3581	GAATGTATTGGGACCTTCCCTGTGAGACCTTTCTAGAGATTAAGAAAGACTACTGGCCTC	3640
Db	3949	GATCATGTTCGGCACTGACCCCGAGAGACCTTTCTGTAGAGAGACACAGAAATGTTAAACTC	4008
Qy	3641	TGTGCAATGGA	3651
Db	4009	TGCATCATGGA	4019
RESULT 15			
ADRI5010	ID	ADRI5010 standard; DNA; 4757 BP.	
XX	AC	ADRI5010;	
XX	DT	21-OCT-2004 (first entry)	
XX	DE	Rat electroconvulsive seizure (EC) signature gene seqid 43.	
XX	KM	neuroleptic; nootropic; antidepressant; eating disorder; tranquilizer;	
XX	KM	neuropsychiatric disorder; signature gene; electroconvulsive seizure;	
XX	KM	ECG; schizophrenia; autism; major depressive disorder; MDD;	
XX	KM	bipolar affective disorder; BAD; psychotic depression; anxiety disorder;	
XX	KM	eating disorder; attention deficit hyperactivity disorder;	
XX	OS	neuropsychiatric drug; gene; ss; rat.	
XX	OS	Rattus norvegicus.	
XX	FN	US2004152107-A1.	
XX	PD	05-AUG-2004.	
XX	PF	18-SEP-2003; 2003US-00664705.	
XX	PR	18-SEP-2002; 2002US-0411718P.	
XX	PR	09-DEC-2002; 2002US-0431882P.	
XX	PR	18-JUN-2003; 2003US-0479970P.	
XX	PA	(AUTA/) ALTAR C A.	
XX	PA	(LAEN/) LAENG P.	
XX	PA	(YOON/) YOUNG T A.	
XX	PI	(CHAR/) CHARLES V D.	
XX	PI	Altar CA, Laeng P, Young TA, Charles VD;	
XX	DR	WPI; 2004-580183/56.	
XX	PT	Identifying compound to treat neuropsychiatric disorder, by contacting	
XX	PT	cell with test compound, determining expression of signature genes by	
XX	PT	cell, comparing expression of signature genes to expression in cell not	
XX	PT	contacted with compound.	
XX	PS	Claim 1; SEQ ID NO 43; 186bp; English.	
XX	CC	The invention describes a method of identifying (M1) a compound to treat	
XX	CC	a neuropsychiatric disorder. The method involves contacting a cell with a	
XX	CC	test compound, determining the expression of one or more signature genes	
XX	CC	by the cell, each signature gene comprising a nucleic acid that	
XX	CC	hybridizes to a nucleic acid chosen from 154 fully defined sequences (S1)	

CC of e.g., 4154, 1582, 645, 367, 405, 1080, 580, 1159, 539, 465, 2002,  
CC 2469, 3155, 421, 2957, 644, 2562, 2858, 1194 and 1227 base pairs as given  
CC in the specification and their complements, and comparing determined  
CC expression of one or more signature genes to expression in cell not  
CC contacted with test compound. Also described are: selecting (M2) one or  
CC more signature genes that are indicative of an effective therapy for  
CC treating a neuropsychiatric disorder; and a kit (I) for detecting an  
CC electroconvulsive seizure (ECS) gene signature, comprising several  
CC oligonucleotides, each of which is capable of specifically hybridizing to  
CC a different ECS signature gene. Therapeutic methods, which use ECS gene  
CC signatures and ECS signature genes to treat, ameliorate or prevent  
CC neuropsychiatric disorders, is also disclosed. (M1) is useful for  
CC identifying a compound to treat a neuropsychiatric disorder chosen from  
CC schizophrenia, autism, major depressive disorder (MDD), bipolar affective  
CC disorder (BAD) and psychotic depression. (M1) is useful for identifying  
CC compounds for treating neuropsychiatric disorders such as anxiety  
CC disorders, eating disorders and attention deficit hyperactivity disorder.  
CC The ECS signature genes of (M1) are useful in diagnostic and prognostic  
CC methods of identifying people who have or who are susceptible to  
CC neuropsychiatric disorders such as MDD and BAD. (M1) enables multi-  
CC parameter high throughput screening of compounds for treating  
CC neuropsychiatric disorders; screening of large number of candidate  
CC compounds for treating neuropsychiatric disorder and enables cost-  
CC effective and rapid screening of compounds useful as neuropsychiatric  
CC drugs. This sequence represents an electroconvulsive seizure (ECS)  
CC signature gene.

XX Sequence 4757 BP; 1122 A; 1288 C; 1197 G; 1150 T; 0 U; 0 Other;

Query Match 61.1%; Score 2264.2; DB 13; Length 4757;

Best Local Similarity 79.5%; Pred. No. 0; Mismatches 618; Indels 134; Gaps 15;

Matches 2919; Conservative 0; Mismatches 618; Indels 134; Gaps 15;

QY 74 GGGCCATGACGACGAGCGCGCGCGAGCTCCGACGAGCGGTAGCGCCCTGTAAAGC 133  
DB 390 GAGCCACCGAGTGGCGCGCTGGCGTATAGAACATGACGCGCCCTTGTGGCTTGAGAGAC 449  
QY 134 GGTTCGCTATGCGGGAACCACTGTGAACCTGCGCGCTCCGGAACACTTGTGCTC--- 190  
DB 450 GGGCCGTGATGTTCCACGCCACTGTGAACCAATTGTGTACGCGCCCACTGCTCAGCCCCAG 509  
QY 191 --CGGACCAAGCTGACCTCTGATTAAGCTGACCTGGGACGCGCCGCAACAAGCCGAGGA 248  
DB 510 CACCGACAGGCTCAGCCTCTGTGTAGCTCTCTCTGGCGGAGCGCATCAGACAC----- 563  
QY 249 GTTAAAGAGACCGGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 308  
DB 564 ---AAGCAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 617  
QY 309 GCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364  
DB 618 TCAGCGTGAAGGAGCAGGACCTGTGACTGACCTGGCAGCTGGGATGTGCGCCCTGGC 677  
QY 365 TAAGGTGACANTGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424  
DB 678 CAGAGTGGACATGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 737  
QY 425 TCTGAGAGGAGCGAGCTTGTGCGCTGTCCAGCTCTGCAATGAGAGGCTCTCGAGTCTGT 484  
DB 738 TCTGAGAGGAGCTTCTTGTGCGCTGTCCAGCTCTGCAATGAGAGCACAATGAGATTGGT 797  
QY 485 GCAAGCGAGCTTCTCTGCGGAGCTGTGGCACTTTCGAGATTGAGAGCTTAACAGTGTAGATC 544  
DB 798 GTACCGAGAGCTTCTCTGCGGAGCTGTGGCACTTTCGAGATTGAGAGCTTAACAGCACTT 857  
QY 545 CTGAGGACATCAACCGAATTTTCAATCGCAACCGAAGAGTTTGAATCATCAACGAG 604  
DB 858 CAGAGGACATCAACCGAATTTTCAATCGCAACCGAAGAGTTTGAATCATCAATGAG 917  
QY 605 ATGATGTTGAAGCTTATGTGGAGCTGAGAAATGTGACAAATGTGGATTCTGAGATTAAAT 664  
DB 918 ATGATGTCGAGAGCTTATGCTGGAGGCTGAAAACTTAACTTGTGATTTCGGGCTTAAAGT 977

QY 665 TTGTGCTCATTAAGCACTTCTGAAAAACGAACTCGACGACATCAATTTTACCGGA 724  
DB 978 TTGTGCTCATTAAGCAAGGCTTCTGAAAAACGAACTCGACGACATCAATTTTACCTGAA 1037  
QY 725 ACAAGTGAAGAGTTGTCTAGAGAACTTTCCGTCACCTTGTGATCTGAACTGATCC 784  
DB 1038 ACAAGTGAAGAGTTGTCTAGAGAACTTTCCGTCACCTTGTGATCTGATCTGATCC 1097  
QY 785 TGTGAGGCAATTCATTTACATGCTCTGTGACATTAATGTGATCAAGACTCTCAAGAGG 844  
DB 1098 TGACGGGTATTCGTTTCAAGTGTCTGTGACATCATGTGAGCTCAAGACTCTCAAGAGA 1157  
QY 845 CTAAATTCAGTCCAGACATCGAGAGTTTGTACTGCTCTGAAATGAACAGAGAAATTTTC 904  
DB 1158 GGAATTCAGGCGCCGACATCAAGATTTGTATGTCTCAATGAGACAGAGAAATTAACC 1217  
QY 905 CCTGCGAAACCTGACAGATPACCAATTTGTGATGTGATGATGATGATGATGATGATGAT 964  
DB 1218 CTGTGCGAAGCTGACAGATTTCCCAATTTGTGTCTGCGCTGTGACGCTTGCCGCTCTA 1277  
QY 965 ACCTCATGTGAGAGAGAGAAAGCTATCACTTATCTGTAGTGTGAGAGTATCCGG 1024  
DB 1278 ACCTCATGAGAGAGAGAGAGAGAGTGTGACATTTCTGTGACAGCTCGGGGAGTACCCGC 1337  
QY 1025 TTCTTAATATATTTGGAGATTTGTGTATCTGTGTTCCAAACATATGATGAAACAAGCC 1084  
DB 1338 TCCCACTTGTATCTGTGAGAGGTTGTGATTTGTTCAAACATGAAATGAACAAGCC 1397  
QY 1085 ACACAGAGGCTCCTTAAGATTAATACTTAATCATCCGATGACAGTGGAGAGAGATCT 1144  
DB 1398 ACACAGAGGCTCCTTAAGATTAATACTTAATCATCCGATGACAGTGGAGAGAGATCT 1457  
QY 1145 CTGTGTGAGGAGAAATCTTGTGAGAGAAAGATCAAGATTTGTCAACTGTGTGATTT 1204  
DB 1458 CTGTGTGAGGAGAAATCTGTGTGAGAGAGATCAAGATTTGTCAACTGTGTGATTT 1517  
QY 1205 TTGACCAACTATCACTTTCTGAAATCTTCGAACCTTCAGACCACTGTGTGATTTCCAT 1264  
DB 1518 TTGACCAACTATCACTTTCTGAAATCTTCGAACCTTCAGACCACTGTGTGATTTCCAT 1577  
QY 1265 TCACTGTAAGAGGCAACCCCAACCAAGCGCTTCAAGTGTCTTAATCAAGGAGCAATTTGA 1324  
DB 1578 TCACTGTAAGAGGCAACCCCAACCAAGCGCTTCAAGTGTGTCTTAATCAAGGAGCAATTTGA 1637  
QY 1325 ATGAGTCCAAATACATCTGTATTAATATCATGTATCAATCAACGAGATACAGGCT 1384  
DB 1638 ATGAGTCCAAATACATCTGTATTAATATCATGTATCAATCAACGAGATACAGGCT 1697  
QY 1385 GCTTCCAGCTGTATTAATCCCATCTCAATGAACATGAGGAGCTACCTTAATAGCCAAAG 1444  
DB 1698 GCTTCCAGCTGTATTAATCCCATCTCAATGAATGAGGAGCTACCTTAATAGCCAAAG 1757  
QY 1445 ATGAGTATGAGGAGAGTATGAGAAACAGATTTCTGCTCACTTCAAGGAGTGGCTGGAATTG 1504  
DB 1758 ATGAGTATGAGGAGAGTATGAGAAACAGATTTCTGCTCACTTCAAGGAGTGGCTGGAATTG 1817  
QY 1505 ACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1564  
DB 1818 ACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1874  
QY 1565 ATGACATCGGAGGAGCAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1624  
DB 1875 ATGACATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1934  
QY 1625 AAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1684  
DB 1935 AAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1994  
QY 1685 TTGAGCTTTGTGATGCTGTGTTCTGCTTAAGTTGAGAGACATCAAGTTTGTGAGTGA 1744  
DB 1995 TCTGCTGCTGTGATGCTGTGTTCTGCTTAAGTTGAGAGACATCAAGTTTGTGAGTGA 2054  
QY 1745 AAGGCCAGGCTTCGTTATCAGGATGATGATGATCTCTGCAAGCCCACTCATCAATCT 1804

Db 2055 AAGGCCAGCTTCGTCATGACAAAGCATGACTTCGCAAGCCCTCTCCACCACT 2114  
Qy 1805 CCAATGGAGATGATCACTCATCTTCTTGGAAGGTGGCCAGATGCTGCTATTTGGA 1864  
Db 2115 CCAAGGGAGACAACTCTCTTCTTGAGGGGGGGCCGATGCTGCTATTTGGA 2174  
Qy 1865 TGACCAAGATCTCTGCTATGAAAATCCCACTTCTTGATCAACCAAGTCACTCA 1924  
Db 2175 TGACCAAGATCTCTGCTATGAAAATCCCACTTCTTGATCAACCAAGTCACTCA 2234  
Qy 1925 AGCCAGACATTTTGTTCAGACATCAAGCAATTAATTTGTGAAAAGGAGCTAG 1984  
Db 2235 AGCCGAGACATTTTGTTCAGACATCAAGCAATTAATTTGTGAAAAGGAGCTAG 2294  
Qy 1985 GCGAAGGAGCTTTGSAAGATGTTCCAGTGAATGTATTAACCTCTGCTGAGCAG 2044  
Db 2295 GAGAAAGGAGCTTTGSAAGATGTTCCAGTGAATGTATTAACCTCTGCTGAGCAG 2354  
Qy 2045 ACAAGATCTTGAGGAGTGAAGACCTGGAAGATGCAATGCAATGCAAGCAAGCT 2104  
Db 2355 ATAAGATCTTGAGGAGTGAAGACCTGGAAGATGCAATGCAATGCAAGCAAGCT 2414  
Qy 2105 TCCACCGTGAAGCGAGCTCTGACCAACTCCAGCATGACACATGCTCAAGTTCTAG 2164  
Db 2415 TCCATCGGAAGCGAGCTGCTGACCAACTCCAGCATGACACATGCTCAAGTTCTAG 2474  
Qy 2165 GCGCTGCTGAGGAGGCGACCCCTCATGATGCTTTGATACATGAAGATGGAGCC 2224  
Db 2475 GTGCTGCTGAGGAGGCGACCCCTCATGATGCTTTGATACATGAAGATGGAGCC 2534  
Qy 2225 TCAACAAGTTCTCTGAGGACACAGGCGCTGATGCGTCTGATGAGGACCAAGCCGC 2284  
Db 2535 TCAACAAGTTCTCTGAGGACACAGGCGCGAATGCAAGTCTGATGAGGACCAAGCCGC 2594  
Qy 2285 CCACGGAATGACGAGTGCAGATGCTGATATAGCCCAAGATGCGCGGAGCATG 2344  
Db 2595 CCACGAGCTGACGAGTGCAGATGCTGATATAGCCCAAGATGCGCGGAGCATG 2654  
Qy 2345 TCTACCTGAGCCTCCAGACATTTGTGCAACCGCATTTGGCCACAGAACTGCTGCTG 2404  
Db 2655 TCTACCTGAGCCTCCAGACATTTGTGCAACCGCATTTGGCCACAGAACTGCTGCTG 2714  
Qy 2405 GGGAGAACTTGTCTGTGAAAATCGGGGACTTTGGGATGTCGGGGAGCTGTACAGACTG 2464  
Db 2715 GAGGAACTTGTCTGTGAAAATCGGGGACTTTGGGATGTCGGGGATGTATACAGCCG 2774  
Qy 2465 ACTACTACAGGATCGTGGCCACAAATGCTGCCATTTGCTGATGCTCCAGAGACA 2524  
Db 2775 ACTACTACAGGATCGTGGCCACAAATGCTGCCATTTGCTGATGCTCCAGAGACA 2834  
Qy 2525 TCAATGATACAGAAATTCACAGCGAAAGCGATGCTGAGCTTGAGGAGCTGCTG 2584  
Db 2835 TCAATGATACAGAAATTCACAGCGAGATGAGTGTGAGCTTGAGGAGCTGCTG 2894  
Qy 2585 AGATTTTCACTTATGAGCAAGCGCTGTACTACAGCTGTCAACATAGAGGTATAGT 2644  
Db 2895 AGATTTTCACTTATGAGCAAGCGCTGTACTACAGCTGTCAACATAGAGGTATAGT 2954  
Qy 2645 GTATCACTCAGGCGGATCTGTCAGCGACCCCGCATGCGCCCGAGAGGTATAGAGC 2704  
Db 2955 GCATCACCGGAGGAGATCTTTCAGGGGCTCGGAGGTGTCCCAAGAGGTATAGAGC 3014  
Qy 2705 TGATGCTGGGGTGTGTCAGCGAAGCGCCCACTAGAGAAATCAAGGCACTCATA 2764  
Db 3015 TGATGCTGGGGTGTGTCAGCGAAGCGCCCACTAGAGAAATCAAGGCACTCATA 3074  
Qy 2765 CCTCTCTTCAAGAACTTGGCCAAAGGATCTCGGTCTACTGCACTTTAGGCTAG--GGC 2823  
Db 3075 CACTCTTTCAGAACTTGGCCAAAGGAGGTGCGCTGTACTGCACTTTAGGCTAGCTC 3134  
Qy 2824 CTTTTTCCGAGCCGATCTTCCCAAGTACTCTCAGACGGGCTGAGAGATGAATCAT 2883

Db 3135 CTTCTTCTCCGAGAGGCGCTTCCCAAGGACCCCTCAGAC----- 3175  
Qy 2884 CTTTAACTGCGCGCTGAGGAGCCAAAGCTCTCTCTTCACTGACAGATTAATCATC 2943  
Db 3176 CTTTAACTGCGCT--GATGACACCACTTGTCTCTCTGCTGACAGGTATAC-- 3232  
Qy 2944 AAAGACTCCGAGAACTCTGAGGAAAGCACTGTGTACTTTGATCCATGACACAGTA 3003  
Db 3233 AGACAGAGAGGCTCTCCGGGGTGAAGCAGTGGCACTTCCCATCCAG--ACAGTA 3290  
Qy 3004 TTGACTCTTTTGGCATATCTCTTCTC----- 3035  
Db 3291 TCGACTGCTTGGCTTTGTGGCTTCTCTCCCTTGTGTTGTTCTTTTGCCCA 3350  
Qy 3036 -----TTTCCATCTCCCTTGGTGTCTTTCTTT 3067  
Db 3351 TTTCTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3410  
Qy 3068 TTTTAAATTTTCTTTCTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 3127  
Db 3411 CTATCTATCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3470  
Qy 3128 CTTTGAATCAATCTGCTTCTGCAATTAATTACTCTGATAGACAAAGCCTTAACA 3187  
Db 3471 CTCTTGAACGATCTGCTTCTGATCTCTATTCATGATCATAGACAAAGCCTTAACA 3530  
Qy 3188 AAGGTAATTTGTATATCAGACACCTCCAGTTTGCACCAACATTAAGCCCTTG 3247  
Db 3531 AACCTGATTTGTATATCAGACACCTCCAGTTTGCACCAACATTAAGCCCTTG 3590  
Qy 3248 TTTGATTTCTGCTTTGATGATGATGAAAAAAGGAAACAAATATTT-----TCACTT 3301  
Db 3591 TTTGATTTCTGCTTTGATGATGATGAAAAAAGGAAATTAATCAACATCTGAC 3650  
Qy 3302 AAACCTTGTCACTTCTGCTGATCAGATATGAGAGTTCTATGATTCATTTAT 3361  
Db 3651 TTTAAACGCTCACTTCCATGATACAGACCGGGGCTTTCTATGATTCATTTAT 3710  
Qy 3362 TTAT-----TATATTACTCTTCTATTTGTTTGGATGCTTATG 3402  
Db 3711 CTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 3770  
Qy 3403 CCTGTATTAATAAAGAAACCTTGTTCATCTGTGAAGCCTTATCTATGGAGATTA 3462  
Db 3771 CTTGTATTAAGAAAGAAATCATGTACAGTCTGGAAAACTTTATCTGTGGAAATG 3830  
Qy 3463 AAACCAAG--GAGAAAGAAATTTATTAAGACGCAATATGGAGAAACAAAGACAAC 3520  
Db 3831 AAACCAAGAAAGGAAAGAAAGCTTATACATTAAGCAGCAGAGATGAGACAGAAAAAC 3890  
Qy 3521 ACTGGATCAGCTGTGTCACTTCTTACTTATAGAAATATCTAGCACTGTTAGCTGGAA 3580  
Db 3891 CATTTGATACGCGAGATCTGCTCTGAT--AGAAAAACCAAGAGCCATGAGCTGAG 3948  
Qy 3581 GAATGATTTGGGACCTTCCCTGAGGACCTTTCTGAGAGTAAAGAAAGTACTGCTC 3640  
Db 3949 GATCATTTGGGACCTGACCCCGAGAGCTTTCTGAGAGGACACAGATTTAACTC 4008  
Qy 3641 TGTGCCATGGA 3651  
Db 4009 TGCATCATGGA 4019

Search completed: February 18, 2005, 12:26:58  
Job time : 2106.06 secs

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 01:09:31 ; Search time 12944.8 Seconds  
(without alignments)  
10900.495 Million cell updates/sec

Title: US-10-645-546-1

Perfect score: 1 ccccccacgcacatcaacaa.....gtagagagcaagaatgcctc 3707

Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1643.2	44.3	3092	3	BC075804 Homo sapi
2	1134.6	30.6	2375	3	AK018789 Mus muscu
3	1133	30.6	2285	3	AK028627 Mus muscu
4	879.2	23.7	1832	3	AK009606 Mus muscu
5	833.4	22.5	996	7	CN802365 IL1LUMIGEN
6	786	21.2	887	5	BK452621 BX452621
7	714.6	19.3	789	4	BI632862 603082428
8	695.8	18.8	880	7	CP410870 CH3H069_H
9	627	16.9	627	9	AY403257 Homo sapi
10	622.6	16.8	846	6	CB521879 UI-M-GVO-
11	611.8	16.5	615	1	AL707530 UI-M-GVO-
12	601	16.2	601	1	AL603196 DKF2P686F
13	600.4	16.2	893	5	BP434087 BP434087
14	585	15.8	893	5	BP250017 BP250017
15	585	15.8	893	5	BP439194 BP439194
16	583	15.7	583	5	BP331207 BP331207
17	583	15.7	583	5	BP346852 BP346852
18	581	15.7	730	6	CD803031 UI-M-GVO-
19	579.8	15.6	798	5	BK411496 BX411496
20	576.8	15.6	644	6	CB450137 704769 MA
21	569.4	15.4	582	4	BP346867 BP346867
22	565.4	15.3	697	4	BG695150 NISC 1V13
23	565.4	15.3	756	5	BU709016 UI-M-EWO-
24	556.6	15.0	723	4	BG923208 602824054

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
BC075804	Homo sapiens	cdna clone IMAGE:4939307, with apparent retained intron.	BC075804	GI:50368967	HTC.	Homo sapiens (human)	Homo sapiens	Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, J., Smalls, D.E., Schmeckel, A., Schein, J.B., Jones, S.J., and Marra, M.A.	Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, J., Smalls, D.E., Schmeckel, A., Schein, J.B., Jones, S.J., and Marra, M.A.

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
BC075804	Homo sapiens	cdna clone IMAGE:4939307, with apparent retained intron.	BC075804	GI:50368967	HTC.	Homo sapiens (human)	Homo sapiens	Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, J., Smalls, D.E., Schmeckel, A., Schein, J.B., Jones, S.J., and Marra, M.A.	Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, J., Smalls, D.E., Schmeckel, A., Schein, J.B., Jones, S.J., and Marra, M.A.

REMARK COMMENT  
NHL-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Series: IRAX Plate: 166 Row: f Column: 18  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 21361305  
 This clone has the following problem: retained intron.

## FEATURES

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## ORIGIN

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 Matches 1706; Conservative 0; Mismatches 3; Indels 41; Gaps 2;

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 Db GCCCCCTGTAAAGCGGTTGCTATGCGGAGCACTGTGAACCTGCGCGTCCGAA 765  
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 Qy 239 GCACCGAGAGTAAAGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 298  
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QY 1739 GCATGAAGG 1748  
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2287 GCATGAAGG 2296

RESULT 2  
AKO18789  
DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500040113 product:DJ245M18.1 (PLACENTAL PROTEIN DIFF40) (FRAGMENT) homolog [Homo sapiens], full insert sequence.

ACCESSION AKO18789  
VERSION AKO18789.1 GI:12858688  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20493374  
PUBMED 11042159

REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed capillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861

REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861

REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBMED 12002159

REFERENCE 6  
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furumori, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaubawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suika, H., Tagami, M., Tagawa, A., Takehashi, F., Tanaka, T., Tejima, Y., Toy, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
Please visit our web site (http://genome.gsc.riken.jp/) for further details.

FEATURES  
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ORIGIN  
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Query Match 30.6%; Score 1134.6; DB 3; Length 2375;  
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Matches 1383; Conservative 0; Mismatches 274; Indels 24; Gaps 6;

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Db 288 CCACGAGTGGTGTGCTGCGATATAGACTATGACGCCCTGTGGCTCGAGAGAGCGGC 347  
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QY 137 TCGGTATCCGGGAGCACTGTGAACCTCGCGCTCGCCGGAACACTTTCGCTC-----C 191  
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Db 348 CCGGATGTCCACACCACTGTGAACCTTGTGTAGGCGCAACCTGTCAAGCCCGCAGAC 407  
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QY 192 GGACAGCTGAGCTCTGATTAAGTGTGAGCTCGGACCGCCGCAACAAGACCGAGGATT 251  
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 Db 1833 GCAATGGGAGCAATCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1892  
 Qy 1688 GCGTTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1747  
 Db 1893 GCGTTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1952  
 Qy 1748 G 1748  
 Db 1953 G 1953

RESULT 3  
 AK028827  
 LOCUS  
 DEFINITION  
 Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732460C10 product:DJ245M18.1 (PLACENTAL PROTEIN DIFP40) (FRAGMENT) homolog (Homo sapiens), full insert sequence.  
 ACCESSION  
 AK028827  
 VERSION  
 AK028827.1 GI:26081044  
 KEYWORDS  
 HTC; CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, J., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
AUTHORS 6 (bases 1 to 2285)  
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shimagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.  
FEATURES  
SOURCE Location/Qualifiers  
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/dev\_stage="10 days neonate"  
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ORIGIN  
Query Match 30.6%; Score 1133; DB 3; Length 2285;  
Best Local Similarity 81.6%; Pred. No. 1.4e-277;  
Matches 1391; Conservative 0; Mismatches 290; Indels 24; Gaps 6;  
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DB 210 CCACCGAGTGTGCTCGGTATAGACTATGACACCGCCTTGTGGCTCGAGGACCGGC 269  
QY 137 TCGCTATGCGGGACCACTGTGAACCTGCGCGCTGCGGAACTCTTGGTC-----C 191  
DB 270 CCGCATGTCCGACGACCTGTGAAACATTTGGTCAAGCCCAACTGTCAAGCCCAAGAC 329  
QY 192 GAACACGCTCAAGCTCTGATTAAGTGAAGTGGGACGCGGCAACAAAGCAAGAGATT 251  
DB 330 CGACAGGCTCAAGCTCTGTAGTCTCACTCGCGGGAG-GCCACACAGACCAAGACGA 388  
QY 252 AAGAGAGCGCAAGCGCAGGAGAGGCTCTCCCGCAGCGGCTGGGGGAAAGCGCGCTGCA 311  
DB 389 AGAGG-----GCGCAGGAGGAGGCTCTCCCGCTCGGCGGGGGA---CGCTGTGCTCA 437

QY 312 GCGCGGACACAGGACT-----CGGCTGGCACTGGCTGTAGGATGTGCTCTGGATTA 367  
DB 438 GCGTAGGAGACACGACTCCGACTACGTAGGCACTGGAGCTGGGATGTGCGCTGGCTGA 497  
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DB 498 AGTGGCATGACCCGCCATGGCGCGGCTTGGGGCTTATGCTGCTGTCTTGGGCTTCT 557  
QY 428 GGAGGGCGGCTTGGCGGTGCCAGTCCGTCGCAATGAGAGCGCTCGAGTCTGGATTCG 487  
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DB 618 CTGAGCTTCTCCAGGACATGCTGGCATTTCCGAGATTGAGACCTTAACAGGCTTAC 677  
QY 548 AGAATATCACGGAATTTTCATGCGAACCAGAAAAGTTAGAAATCATCAACGAAATG 607  
DB 678 AGAATATCACGGAATTTTCATGCGAACCAGAAAAGTTAGAAATCATCAATGAAATG 737  
QY 608 ATGTTGAAGCTTATGCGGATCGAGAAATCTGACAAATTTGAGATTCTGATTAATAATTG 667  
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QY 728 AACTGACGAGTTTGTCTAGGAAACATTTCCGTCACTTGAATCTGACATGATCTCG 787  
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DB 918 CGGGTAATCTCGTTACGCTCTCTGACATCAATGATGCTCAAGCTTCCAGGAGACTA 977  
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DB 978 AATCGAATCCAGACACTGAGATTTGTACTCTGTAATGAAAGCGCAAAATTTCCG 1037  
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QY 968 TCACCTGTGAGAGAAAGAAAGCTCTATCACATTTATCTGATGTGCGAGGTATCCGCTTC 1027  
DB 1098 TCACCTGTGAGAGAAAGAAAGCTCTGACCTTCTCTGAGTGTGCGGCTGACCCACTCC 1157  
QY 1028 CTAAATGATTTGGAGTGTGATGTAACCTGTTTCCAAACATATGAAACAAAGCACA 1087  
DB 1158 CCACCTGTACTGGAGCTTGGAAATTTGTTTCCAGACATGATATTAACAGCCACA 1217  
QY 1088 CACAGGGCTCTTAAAGATTAATACTTATCGATCGATGACGTGGAGAGAGATCTCTT 1147  
DB 1218 CACAGGGCTCTTAAAGATTAATACTTATCGATCGATGACGTGGAGAGAGATCTCTT 1277  
QY 1148 GTGTGGCGGAAATCTGTAGAGAAATCAAGATTTCTGTCAACTCACTGTGACTTTTG 1207  
DB 1278 GTGTGGCGGAAATCTGTAGAGAAATCAAGATTTCTGTCAACTCACTGTGACTTTTG 1337  
QY 1208 CACCAATATCACTTTCTGAAATCTCAACCTGACCAACCACTGCGGCAATTCATTTCA 1267  
DB 1338 CCGCAATATCACTTTCTGAAATCTCAACCTGACCAACCACTGCGGCAATTCATTTCA 1397  
QY 1268 CTGTGAAAGGACCCCAACCAAGCTTCTAGTGTCTTATTAAGCGGCAATTTGAATG 1327  
DB 1398 CTGTGAAAGGACCCCAACCAAGCTTCTAGTGTCTTATTAAGCGGCAATTTGAATG 1457  
QY 1328 AGTCCAAATATCATCTGTAATAATTAATTTACATTTACCAATCACAGGAGTACCAAGCTGCC 1387  
DB 1458 AGTCCAAATATCATCTGTAATAATTAATTTACCAATTTACCAATTTACCAATTTACCA 1517

Qy	1388	CCGAGCTGGATATATCCCATCAATGAACATGGGACTACACTTAAATACCAAGATG	1447
Db	1518	TCACGCTGGATACCCCATCATATGAATAAACGAGACTAACCCCTGATGGCCAAAGC	1577
Qy	1448	AGATAGGAAGATAGAGAAAGAGATTTCTGCTCACTTATGAGGCTGGCTGGAATTGACG	1507
Db	1578	AGTATGGAAAGATAGAGACAGATCTCCGCTCACTTCAATGGCCGGCTTGAGTCACT	1637
Qy	1508	ATGTGCAACCCCAATTATCTCTGATGTAAATTATGAAGATTATGAACCTGACAGCATG	1567
Db	1638	ACGAGACAAACCCAAATTACCTCGTAAGTCTCTATGAAGACT---GGACCAACGCCAATCG	1694
Qy	1568	ACATTCGGGACACACCAAGACAGATATGAAAATCCCTTCACACAGACTCATGTAAAA	1627
Db	1695	ACATTGGGGATATCTACAGAACAAAGTATGAAATCCCTCCACAGATGTTCCTACCAAA	1754
Qy	1628	CCGGTCGGGACATCTCTCGGCTATAGCTGATGGTGTATTTGGCTGTGGTGGGATTTT	1687
Db	1755	GCAATCGGAGACATCTCTCGGCTATATGCCGTGGTGGTATTTGCATCTGTGGTGGGATTTCT	1814
Qy	1688	GCCTTTGGTATAGCTGTTTCTGCTTAAGTTGGCAAGCACTCCAAAGTTTGGATGAAAG	1747
Db	1815	GCTGCTGTGATGTGTGCTCCGCTCAAGTTGGCGACGACATTCCAAAGTTTGGCATGAAAG	1874
Qy	1748	GCCCAAGCTCCGTTATACGCAATGA	1772
Db	1875	GAGGAAAGCGCTGATTTATGATGA	1899

RESULT 4	
AC009606	
LOCUS	AK009606 1832 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310034C05 product:DJ245M18.1 (PLACENTAL PROTEIN DIFF40) (FRAGMENT) homolog [Homo sapiens], full insect sequence.
ACCESSION	AK009606
VERSION	AK009606.1 GI:12844502
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency cap-trapping cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	
AUTHORS	2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	
AUTHORS	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsuana,T., Teshiro,H., Itoh,M., Sunf,N., Ishii,Y., Nakamura,S., Hazama,M., Niimine,T., Harada,A., Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawat,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection

JOURNAL	Nature 409,	685-690	(2001)
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
TITLE	Nature 420,	563-573	(2002)
JOURNAL	6 (bases 1 to 1832)		
REFERENCE	Addchi,J., Aizawa,K., Akahira,S., Aktamura,T., Arai,A., Aono,H., Arkkava,T., Bomo,H., Carninci,P., Fukuda,S., Fukushima,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hitachi,T., Horii,F., Imocani,K., Ishii,Y., Itch.M., Izawa,M., Kasukawa,T., Kato,H., Kawari,J., Koijima,Y., Komno,H., Koude,M., Koya,S., Kuhihata,C., Matsuyama,T., Miyazaki,A., Nishil.K., Nomura,K., Numasaki,R., Ono,M., Okazaki.Y., Oikido.T., Owa.C., Saito.H., Saito.R., Sakai,C., Sakai,K., Sano,H., Saeki,D., Shibata,K., Shibata,Y., Shingawa.A., Shiraki,T., Sugabe,Y., Suuki,H., Tagami,M., Tagawa,A., Takahashi.F., Tanaka,T., Yoshino,Y., Toya,T., Yamamori,T., Yasunishi,A., Yoshiida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JULY-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:+81-45-503-9222, Fax:81-45-503-9216)		
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> ) for further details.		
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGACATCCCAAGACTCTTTTITTTTTTYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGCATTCGCAGTAATTAAATAAATCACC(CCCC 3'). cDNA was cleaved with XhoI and NotI. Cloning sites, 5' end: XhoI, 3' end: NotI. Host: SOBR.		
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Dd	9 CTGACTGGACATGGACACTGGGATGTCTCTTGCTGAAGTGGCATGGACCCGCCATNG 68		
OY	CGGGGTCTGGGGCTTCTCTGCTGGCTGTGTGGCTTCTGGAGGGCCGCTTGGCTGTC 448		
Dd	69 CGGGGTCTGGGGCTTCTGCTGTGTGGCTTCTGGAGGGCCCTTCTGGCTGTC 128		
OY	CACGGTCTGGAATGTAGTGCTCTCTGGATCTGATGTCAGAGAACCTTCTCTGGATCG 508		

D	b	129	CGACGTCCTGCAAAATGCAGTTCCGCTTAGGATTTGGTGTACTAGGCTTCTCCAGGATCG	188
Q	y	509	TGGCATTTCCGAGATTGGAGCCTAACAGGTGATCTCTGAGAAATCACCGAAATTTTCA	568
D	b	189	TGGCATTTCCGAGGTTGGAACTTAACAAGGTGTGACCCGGAGAAATCAAGAAATTTCTCA	248
Q	y	569	TCCGAAACCAAAAAAGTTTAAATATCATCAAGAAATGATGTTGAAGCTTATGTGGAC	628
D	b	249	TTGCAAAACAGAAAAAGGCTAGAAATCATCAAGAAATGATCGTTGAGGCTTACGTGGGCG	308
Q	y	629	TGAGAAATCTGACAAATTGAGATTCGTGATTAAATTTGTGGCTCAATAAGATTTCTGA	688
D	b	309	TGAGAAACCTTACAAATTGTGATTCGGCTTAAAGTTTGTGCTTACAAAGGCTTTCTGA	368
Q	y	689	AAAACAGCAACCTGACGACATCAATTTTACCGGAAACAAACCTGACGAGTTGTCTAGGA	748
D	b	369	AAAACAGCAACCTGACGACATCAATTTTACAGAAACAAAGCTGACGAGTTGTCTAGGA	428
Q	y	749	AACATTTCCGTCACTTGACTTGTCTGAACTGATCTCTGTGGGCAATCCATTTACATGCT	808
D	b	429	GACATTTCCGCACTTGAATCTGTCTGAACCTGATCTCTGCGGGTAACTCGTTCACTGCTC	488
Q	y	809	CCTGGAATTAATGAGATTCACATCTTCCAGAGGCTTAAATCCAGTCCAGACCTCAAG	868
D	b	489	CCTGGAATTAATGAGATTCACATCTTCCAGAGGCTTAAATCCAGTCCAGACCTCAAG	548
Q	y	869	ATTGTATCTGCTGATATGAAGAAGCAGAAATATTTCCCTGCGAAACCTGACAGATACCA	928
D	b	549	ATTGTATCTGCTGATATGAAGAAGCAGAAATATTTCCCTGCGAAACCTGACAGATACCA	608
Q	y	929	ATTGTGTTGCCATCTGCAAAATCTGCGCCGACCTTAACTCACTGTGAGAGAAAGAGT	988
D	b	609	ATTGTGTTGCCATCTGCAAAATCTGCGCCGACCTTAACTCACTGTGAGAGAAAGAGT	668
Q	y	989	CTATCACTTATTCCTGTATGAGGAGAGATCCGGTTCCTTAATATGTAATTTGGATdTGG	1048
D	b	669	CTGATACCTTTCCGAGGTGGGGGGGGA--CAACTCCCACTTGTATCTGAGAGGTTG	727
Q	y	1049	GTAACCTGTTTCCAAATATGATGAAACAAAGCACACAGAGGCTCTTAAAGGATTA	1109
D	b	728	GGAATTTGGTTT--CAAGACATGAAATG--GACAAAGCACACAGGGCTCTTAAAGG--	780
Q	y	1109	CTAACATTTTCAATCCGATGACAGTGGGAAAGCAGATCTCTGTGTGGCGGAAATCTTGTAG	1166
D	b	781	-----ATTAACGACATTTTCACTGATGACAGTGAAGCAATCTGTGTGGCAGAAACTTGTAG	835
Q	y	1169	GAGAAAGATCAAGATTTCTGCAACCTCACTGTGATTTTGCACCACTATCAATTTCTG	1228
D	b	836	GAGAAAGAT--AAGATTTCTGTGA--CTCACTGTGATTTTGCAGCACTATCAAGATTTCTG	892
Q	y	1229	AATCTCCAACTCAGACCACTGCTGTGATTCATTTCACTGTGAAAGGCAAC--CCGAA	1288
D	b	893	TATCTCCAACTCAGATCA--CACTGTGATGCAATTTCACTGTGAAAGGCAACGCTTCAAG	950
Q	y	1288	CCAGGCTTTC--AGTGTCTTATTAACGGGCAATATTTGAATGATCCAAATACATCTGTAC	1344
D	b	951	CTGTGGCTTCAAGTGTGTCTTAACAATGGGGGCAATCTGAGTGAAGTCCGAGTACATCTGTAC	1011
Q	y	1344	TAAATACATGTTACCAATCAACGAGAGTACCAAGGCTGCTCCAGCTGATATATCCAC	1400
D	b	1011	TAAATACATGTTACCAATCAACGAGAGTACCAAGGCTGCTCCAGCTGATATATCCAC	1071
Q	y	1407	TCACATGAACAATGGGGACTAACCTCTTAAATACCAAGAAATGATGGAAGGATGAGAA	1466
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Q	y	1467	ACAGATTTCTGCTCACTTCATGAGGCTGGCTGGAATTTGACATGAGTGTGCAAAACCAATTA	1522
D	b	1131	ACAGATTTCTGCTCACTTCATGAGGCTGGCTGGAATTTGACATGAGTGTGCAAAACCAATTA	1199
Q	y	1527	TCCTGATGTAATTTATGAAGATTTATGAACTGACAGGAATGACATCTGGGGACACCAAGAA	1588

Df		1191	CCGGAAGTCTCATTATGAAGA-CT---GGACACAGGCCAACTGCATTTGGGGATACTAACATA	1247
OY		1587	CAGAAGTAATGAATTCCTTCCACAGACGTCACTGATTAACAACGGGTGGGAACATCTCTC	1646
Df		1248	CAAAAAGTAATGAATATCCCCTCCACGGAGATGTTCGACCAAAGCAATCGGGGCATCTCTC	1307
OY		1647	GGCTATAGCTGTGTGTGGATGTGCCTGTGTGTGTGGATTTTTTGCTTTTGGTAAGCTGTT	1706
Df		1308	GGTATAGCCCGTGTGTGGATGTGATCTGTGTGTGTGGATTTCTGTCTGCTGTGTGTGTGCT	1367
OY		1707	TCTGCTTAAGTTGGCAAGACACTCCAAGTTTGGCATGAAGG	1748
Df		1368	CTCTCTCAAGTTGGCGAGACATTTCCAAAGTTTGGCATGAAGG	1409
RESULT 5				
CN802365/c				
LOCUS				
DEFINITION		CN802365	996 bp mRNA linear EST 26-MAY-2004	
		ILLUMIGEN MCO 38167 Katze_MMR Macaca mulatta cDNA clone		
		IBUW:14671.5 similar to Baes 1 to 980 highly similar to human		
		NTRK2 (Hs:439109), mRNA sequence.		
ACCESSION		CN802365		
VERSION		CN802365.1 GI:47698341		
KEYWORDS		EST.		
SOURCE		Macaca mulatta (rhesus monkey)		
ORGANISM		Macaca mulatta		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
JOURNAL		Cercopithecinae; Macacae.		
COMMENT		1 (bases 1 to 996) Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L. Large-scale Rhesus Macaque cDNA Sequencing Unpublished (2003) Contact: C. Magness Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel.: 2063780400 Fax: 2063780408 Email: cmagness@illumigen.com Sequenced on 2004.05.18. 675 Q20 bases. PCR primers FORWARD: CCTCACATAAAGGAAACAAA BACKWARD: CACTATAGGCGCATTTGGGTA Insert Length: 996 Std Error: 0.00 Plate: CL000274 row: C column: 02 Seq primer: CCTCACATAAAGGAAACAAA POLYA=No.		
FEATURES				
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		/sex="female"		
		/dev stage="adult"		
		/lab host="E. coli SOLR"		
		/clone lib="Katze_MMR"		
		/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I; Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (catalog #200450)"		
ORIGIN				
Query Match		22.5%	Score 833.4;	DB 7;
Best Local Similarity		92.4%	Pred. No. 3.8e-201;	Length 996;
Matches		Conservative	0;	Mismatches 71;
				Indels 4;
				Gaps 3;
OY		328	TGGGAGTGGCACTGGCTGTGATGATTCGCTCGATTAAGTGGCATGACCAGCATG	387
Df		981	TGGGAGTGGCCCCCTGTGTATGAGGAATTTTCCTCGATAAG--GGGAGGAGACCGCCAGG	924
OY		388	GCGCGGCTCTGGGCGCTTCTGCTGGCTGTGTGTGGGCTTTGAGAGGCGCGCTTTCGCTGT	447



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Db 923 GCGGGG-TTTGGGGCTTTGCTGCTGTTTGGGTTTGA-GGCGGGCTTGTCTGT 866
Qy 448 CCCAGCTCTGCAATGAGTGCCTCTGGATCTGGTGACGACCCCTTCTCTGGCATC 507
Db 865 TCCAGCTCTGCAATGAGTGCCTTCTGGATCTGGTGACGACCCCTTCTCTGGCATC 806
Qy 508 GTGGCAATTCGGAATGGAGCTTACAGGTGTATCTCTGGAACATCACCGAAATTTTC 567
Db 805 CGTGGCAATTCGGAATGGAGCTTACAGGTGTATCTCTGGAACATCACCGAAATCTTC 746
Qy 568 ATCCGAACACGAAAGGTTAGAAATCATCAACGAAGTATGTTGAAGCTTATGTGGGA 627
Db 745 ATCCGAATTCGAAAGGTTAGAAATCATCAACGAAGTATGTTGAAGCTTATGTGGGA 686
Qy 628 CTGGAAGATCTGACATTTGTGGATTTGATTAATTTGTGCTCAAAAGCATTTCTG 687
Db 685 CTGGAAGATCTGACATTTGTGGATTTGATTAATTTGTGCTCAAAAGCATTTCTG 626
Qy 688 AAAAAACGCAACCTGACGACATCAATTTTACCAGAAACAACTGACGAGTTGTCTAG 747
Db 625 AAAAAACGCAACCTGACGACATCAATTTTACCAGAAACAACTGACGAGTTGTCTAG 566
Qy 748 AAACATTTCCGTGACCTTGACTTGTCTGAATCTGCTGGTGGGCAATTCATTAATGC 807
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Qy 808 TCTGTGACATTAATGTGATCAAGCTCTCCAGAGGCTAAATCCAGTCCAGACATCAG 867
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Qy 868 GATTGTGATGCTGCTGATGAAAGCAAGAAATTTCCCTGCGAAACCTGACATGCC 927
Db 445 GATTGTGATGCTGCTGATGAAAGCAAGAAATTTCCCTGCGAAACCTGACATGCC 386
Qy 928 AATTGTGATGCTGCTGATGAAATCTGGCGCACCTAACTCAGTGTGAGAGAGAAAG 987
Db 385 AATTGTGATGCTGCTGATGAAATCTGGCGCACCTAACTCAGTGTGAGAGAGAAAG 326
Qy 988 TCTATCAATTAATCTGTAGTGTGAGAGTATCCGTTCTTAATATGTATGTGGATGTT 1047
Db 325 TCTATCAATTAATCTGTAGTGTGAGAGTATCCGTTCTTAATATGTATGTGGATGTT 266
Qy 1048 GGTAACTGCTGCTGCTGATGAAATCAATGAAACCAAGCCACACAGGCTCTTAAGATA 1107
Db 265 GGTAACTGCTGCTGCTGATGAAATCAATGAAACCAAGCCACACAGGCTCTTAAGATA 206
Qy 1108 ACTAACTGCTGCTGCTGATGAGTGGAGAGAGATCTTGTGTGGCGGAAATCTTGTGA 1167
Db 205 ACTAACTGCTGCTGATGAGTGGAGAGAGATCTTGTGTGGCGGAAATCTTGTGA 146
Qy 1168 GGAAGAGTCAAGATTTCTGTCACTCACTGTGATTTTGACCAACTATCAATTTCTC 1227
Db 145 GGAAGAGTCAAGATTTCTGTCACTCACTGTGATTTTGACCAACTATCAATTTCTC 86
Qy 1228 GAATCTCCAACTCAAGACCACTGCTGATTTTCACTGTTGAAAAGCAACCCCAA 1287
Db 85 GAATCTCCAACTCAAGACCACTGCTGATTTTCACTGTTGAAAAGCAACCCCAA 26
Qy 1288 CCAAGCGCTGAGTGTCTATTAAG 1312
Db 25 CCAAGCGCTGAGTGTCTATTAAG 1

RESULT 6
LOCUS BX452621 887 bp mRNA linear EST 06-MAY-2004
DEFINITION BX452621 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
            CS0DN003YE01 5-PRIME, mRNA sequence.
ACCESSION BX452621
VERSION BX452621.2 GI:47065467
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 887)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31028369.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5428.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=0BA00712A08_CS06777_2ac=5428.f

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN003YE01"
/issue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match 21.2%; Score 786; DB 5; Length 887;
Best Local Similarity 96.9%; Pred. No. 4.8e-189;
Matches 812; Conservative 0; Mismatches 25; Indels 1; Gaps 1;
Qy 36 GAGAGTCCCGAGCGCGCGGTGTCGCCGCGCGCGCGGCAATGAGGAGCGCGCGC 95
Db 1 GAGTCCCGAGCGCGCGGTGTCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 60
Qy 96 GCGAGCTCCGAGGAGCGGTAGCGCCCGCTGTAAAGCGGTCTGCTATGCGGAGCACT 155
Db 61 GCGAGCTCCGAGGAGCGGTAGCGCCCGCTGTAAAGCGGTCTGCTATGCGGAGCACT 120
Qy 156 GTGAACCTGCGCGCTGCGGAAACATCTTGTGCTCCGACCAAGCTCAAGCTGTATAGC 215
Db 121 GTGAACCTGCGCGCTGCGGAAACATCTTGTGCTCCGACCAAGCTCTGTATAGC 180
Qy 216 TGGACTGGGACCGCCGCAACAGCAACGAGAGTTTAAAGAGCGGAAAGCGGAGGA 275
Db 181 TGGACTGGGACCGCCGCAACAGCAACGAGAGTTTAAAGAGCGGAAAGCGGAGGA 240
Qy 276 GCTCCCGGACGAGGTGGGAGAAAGCGCGGTGACAGCGGAGGAGCAAGCACTGGGCTG 335
Db 241 GCTCCCGGACGAGGTGGGAGAAAGCGCGGTGACAGCGGAGGAGCAAGCACTGGGCTG 300
Qy 336 GCACTGCTCTAGAGATGTGCTCTGGAATTAAGTGAATGAGACCGGCATAGCGGCT 395
Db 301 GCACTGCTCTAGAGATGTGCTCTGGAATTAAGTGAATGAGACCGGCATAGCGGCT 360
Qy 396 CTGGAGGCTTCTGCTGAGTGTGTTGGGCTTCTGAGAGGCGCGCTTCCCTGTCCACGTC 455
Db 361 CTGGAGGCTTCTGCTGAGTGTGTTGGGCTTCTGAGAGGCGCGCTTCCCTGTCCACGTC 420
Qy 456 CTGCAATGCAAGTCTCTGATCTGTGCAAGCACTTCTCTGAGCATGTGGCATTT 515
Db 421 CTGCAATGCAAGTCTCTGATCTGTGCAAGCACTTCTCTGAGCATGTGGCATTT 480
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QY 516 TCCGAGATTGGAGCCTTAACAGTGTAGATCTGAGAACATCCAGAAATTTTCATCGCAA 575  
 Db 481 TCCGAGATTGGAGCCTTAACAGTGTAGATCTGAGAACATCCAGAAATTTTCATCGCAA 540  
 QY 576 CCAGAAAAGGTAAAGATCAACAGAGATGATCTTAAGCTTAATGTGGAGCTGAGAA 635  
 Db 541 CCAGAAAAGGTAAAGATCAACAGAGATGATCTTAAGCTTAATGTGGAGCTGAGAA 600  
 QY 636 TCTGACAAATGTGATTTGATTTAAATTTGTGGCTCATTAAGCATTTCTGAAAAACAG 695  
 Db 601 TCTGACAAATGTGATTTGATTTAAATTTGTGGCTCATTAAGCATTTCTGAAAAACAG 660  
 QY 696 CAACCTGACAGACATCAATTTTACCCGAAACAACTGACGAGTTTGTCTAGAAAACATTT 755  
 Db 661 CAACCTGACAGACATCAATTTTACCCGAAACAACTGACGAGTTTGTCTAGAAAACATTT 720  
 QY 756 CCGGACCTTGAATCTTGTGAACTGATCTGTGTGGCAATTCATTTAAATGCTCTGTGA 815  
 Db 721 CCGGACCTTGAATCTTGTGAACTGATCTGTGTGGCAATTCATTTAAATGCTCTGTGA 780  
 QY 816 CATTATGTGATCAAGACTCTCAAGAGAGC-TAAATCCAGTCCAGACATCGAGATTT 872  
 Db 781 CATTATGTGATCAAGACTCTTAAAGAGGCTTAAATCCAGTCCAGACCTCAAGATTT 838  
 RESULT 7  
 B1832862 789 bp mRNA linear EST 04-OCT-2001  
 LOCUS 60308242861 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5221663 5'  
 DEFINITION mRNA sequence.  
 ACCESSION B1832862  
 VERSION B1832862.1 GI:15944412  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 789)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgsrpb@rmail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMNI at:  
 http://image.llnl.gov  
 Plate: LAM11557 row: g column: 08  
 High quality sequence scop: 788.  
 Location/Qualifiers  
 1. 789  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5221663"  
 /lab\_host="DH10B"  
 /clone\_id="NIH\_MGC\_120"  
 /note="Organ: pooled pancreas and spleen; Vector:  
 PCWV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of spleen and pancreas from 28 yo  
 male. Library is oligo-dT primed and directionally cloned  
 (EcoRV site is destroyed upon cloning). Average insert  
 size 1.5 kb, insert size range 1-2.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 025. Note: this is a NIH\_MGC Library."  
 ORIGIN  
 Query Match 19.3%; Score 714.6; DB 4; Length 789;  
 Best Local Similarity 97.6%; Pred. No. 8.1e-171;

Matches 768; Conservative 0; Mismatches 14; Indels 5; Gaps 4;  
 QY 184 TTCGCTCCGAGCAGACTCAGCCTCTGATTAAGCTGAGACTCGGACGCGCAACAGCACC 243  
 Db 1 TTCGCTCCGAGCAGACTCAGCCTCTGATTAAGCTGAGACTCGGACGCGCAACAGCACC 60  
 QY 244 GAGGAGTTAAGAGAGCGGCAAGCGGAGGAGGCTCCCGGACGCGTGGGGGAAAGCGG 303  
 Db 61 GAGGAGTTAAGAGAGCGGCAAGCGGAGGAGGCTCCCGGACGCGTGGGGGAAAGCGG 119  
 QY 304 CCGGTGACGCGCGGGGACAGGCACTTGGGGCTGGGACTGCTGATGAGATTCGCTCGG 363  
 Db 120 CCGGTGACGCGCGGGGACAGGCACTTGGGGCTGGGACTGCTGATGAGATTCGCTCGG 179  
 QY 364 ATAAGTGGCATGAGACCGCATGAGCGGCTCTGGGGCTTCTGCTGCTGAGTTGGGC 423  
 Db 180 ATAAGTGGCATGAGACCGCATGAGCGGCTCTGGGGCTTCTGCTGCTGAGTTGGGC 239  
 QY 424 TTCTGAGGGGCGGCTTTGCGCTGTCGACGCTCTGCAATGCAAGTCCCTCGATCTGG 483  
 Db 240 TTCTGAGGGGCGGCTTTGCGCTGTCGACGCTCTGCAATGCAAGTCCCTCGATCTGG 299  
 QY 484 TGCAGCGACCTTCTCTCTGAGATGCTGGCATTTCCGAGATTGGAGCTTAACAGTAAAT 543  
 Db 300 TGCAGCGACCTTCTCTCTGAGATGCTGGCATTTCCGAGATTGGAGCTTAACAGTAAAT 359  
 QY 544 CCTGAGAACATCACCGAAATTTTCATGCGCAACGAGAAAGGTTAGAAAT--CATCAAG 601  
 Db 360 CCTGAGAACATCACCGAAATTTTCATGCGCAACGAGAAAGGTTAGAAATTCATCAAG 419  
 QY 602 AAGATG-ATGTTGAAGCTTATGTGGGACTGAGAAATCTGACAAATTTGATTTGATTA 660  
 Db 420 AAGATGATGTGGAAGCTTATGTGGGACTGAGAAATCTGACAAATTTGATTTGATTA 479  
 QY 661 AATTTTGGCTCATTAAGCATTTTCTGAAAAACGCACTGCGACATCATTAATTTTACC 720  
 Db 480 CAATTTGGCTCATTAAGCATTTTCTGAAAAACGCACTGCGACATCATTAATTTTACC 539  
 QY 721 CGAAACAACATGAGAGTGTGTAGAGAAATTTCCGTCACCTTGACTGTGGAATCG 780  
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 QY 781 ATTCGTGGGCAATTCATTTACATGCTCTGTGACATTTATGTGATCAAGACTCTCCAA 840  
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 QY 841 GAGGCTAATTCAGTCCAGACACTGAGATTTGTACTGCTGAATGAAAGAGC-AGAA 899  
 Db 660 GAGGCTAATTCAGTCCAGACACTGAGATTTGTACTGCTGAATGAAAGAGC-AGAA 719  
 QY 900 TATTCCTCGGCAAACTGCGAGATACCAATTTGTGTTGGCATCTGCAATTCGGCGCG 959  
 Db 720 TATTCCTCGGCAAACTGCGAGATACCAATTTGTGTTGGCATCTGCAATTCGGCGCG 779  
 QY 960 ACTTAAC 966  
 Db 780 ACTTAAC 786  
 RESULT 8  
 CF410870 880 bp mRNA linear EST 02-SEP-2003  
 LOCUS CF410870  
 DEFINITION CH3#069\_H10MF Canine heart normalized cDNA library in pbucscript  
 Canis familiaris cDNA clone CH3#069\_H10 5', mRNA sequence.  
 ACCESSION CF410870  
 VERSION CF410870.1 GI:34412116  
 KEYWORDS EST.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.  
 1 (bases 1 to 880)  
 Yi,Y., Desai,R., Olathe,M., Henthorn,P. and George A.L.

TITLE Expressed sequence tags from Canine heart  
JOURNAL Unpublished (2003)  
COMMENT Other ESTs: CH3#069\_H10MR  
Contact: George AL  
Division of Genetic Medicine  
Vanderbilt University  
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA  
Tel: 615 936 2660  
Fax: 615 936 2661  
Email: al.george@vanderbilt.edu  
Insert Length: 2013 Std Error: 0.00  
Seq primer: MF: GTTTCCTCCAGTCAGCAGCTTG  
High quality sequence start: 83  
High quality sequence stop: 788.  
Location/Qualifiers  
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/clone="CH3#069\_H10"  
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/cell\_type="heart"  
/dev\_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"  
/clone\_lib="Canine heart normalized cDNA library in pBluescript"  
/note="Organ: heart; Vector: pBluescript; Site: 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dt primed"

ORIGIN  
Query Match 18.8%; Score 695.8; DB 7; Length 880;  
Best Local Similarity 91.9%; Pred. No. 5.3e-166; Indels 0; Gaps 0;  
Matches 733; Conservative 0; Mismatches 65;

442 GCCTGTCCACAGCTCTGCAAAATGACAGTCTCTCGATCTGTGACAGCCTTCTCTCT 501  
83 GCTGTCCACAGCTCTGCAAAATGACAGCCTCTGATCTGTGACAGCCTTCTCTCTCG 142

502 GGCATCTGCGCATTTCCGAGATTGAGAGCTTAACAGTGAATCTTGAGAAATCAACCGAA 561  
143 GGCATCTGCGCATTTCCGAGATTGAGAGCTTAACAGTGAATCTTGAGAAATCAACCGAA 202

562 ATTTCATCGCAAAACAGAAAGGTTAGAAATCATCAAGAGATGATGTTGAAGCTTAT 621  
203 ATTTCATCGCAAAACAGAAAGGTTAGAAATCATCAAGAGATGATGTTGAAGCTTAT 262

622 GTGGAGCTGAGAAATCTGACAATTGTGATTTCTGATTTAAATTGTGGCTCATTAAGCA 681  
263 GCAAGATTGAAGAAATCTGACATTGTGACCTTGATTTAAATTGTGGCTCATTAAGCA 322

682 TTTCTGAAAAACAGCAACTGACACATCAATTTTACCGAAACAACTGACAGATTG 741  
323 TTTCTGAAAAACAGCAACTGACACATCAATTTTACCGAAACAACTGACAGATTG 382

742 TCTAGAAAAACATTTCCGTCACCTTGAATTTGCTGAACGATCTGTGGGGCAATCCATT 801  
383 TCTAGAAAAACATTTCCGTCACCTTGAATTTGCTGAACGATCTGTGGGGCAATCCATT 442

802 ACATGCTCTCTGACATTATGTGATCAAGACTCTCCAAAGAGCTAAATCCAGTCCAGAC 861  
443 ACATGCTCTCTGACATTATGTGATCAAGACTCTCTCCAAAGAGCTAAATCCAGTCCAGAA 502

862 ACTGAGATTGTAATGCTGTAATGAAGAGCAAGAAATTTCCCTGGCAAACTGACAG 921  
503 ACTGAGATTGTAATGCTGTAATGAAGAGCAAGAAATTTCCCTGGCAAACTGACAG 562

922 ATACCCAAATGTGTTGGCATCTGCAAAATCTGGCCGACCTTAACCTCACTGTGAGAGAA 981  
563 ATACCCAAATGTGTTGGCATCTGCAAAATTTGGCTGCACTTAACCTCACTGTGAGAGAG 622

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DB 683 GATGTTGGTACCTGGCTTCCAAACATATGAAATGAAGAACAGCCACAGAGGGCTCCTTG 742

QY 1102 AGGATTAATACTAATTTATCTGATGATGAGAGTGGAGAGAGATCTTGTGTGGCGAAAT 1161  
DB 743 AGGATTAATACTAATTTATCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 802

QY 1162 CTGTGAGAGAGAGATCAAGATTTCTGTACACTCACTGTGATTTTGAACCAATATGACA 1221  
DB 803 CTGTGAGAGAGAGATCAAGATTTCTGTACACTCACTGTGATTTTGTCTCAATATGACA 862

QY 1222 TTTCTGGAATCTCCAAAC 1239  
DB 863 TTTCTGGAATCTCCAAAC 880

RESULT 9  
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LOCUS AY403257  
DEFINITION Homo sapiens HCM1497 gene, VIRUAL TRANSCRIPT, partial sequence,  
ACCESSION AY403257  
VERSION AY403257.1 GI:39759240  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

TITLE JOURNAL  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 627)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
JOURNAL  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
SOURCE  
1. .627  
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/db\_xref="taxon:9606"  
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/locus\_tag="HCM1497"

ORIGIN  
Query Match 16.9%; Score 627; DB 9; Length 627;  
Best Local Similarity 100.0%; Pred. No. 1.8e-148; Indels 0; Gaps 0;  
Matches 627; Conservative 0; Mismatches 0;

QY 2194 ATGGTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2253  
DB 1 ATGGTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60

QY 2254 GATGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2313  
DB 61 GATGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

QY 2314 CATATAGCCAGAGATGCGCGCGCATGTCTACCTGCGCTGCCAGCACTTGTCAC 2373  
DB 121 CATATAGCCAGAGATGCGCGCGCATGTCTACCTGCGCTGCCAGCACTTGTCAC 180  
QY 2374 CGCATTTGGCCACACAGAACTGCTGTCGGGGAACTTGTGTGTAATAATGGGGAC 2433  
DB 181 CGCATTTGGCCACACAGAACTGCTGTCGGGGAACTTGTGTGTAATAATGGGGAC 240  
QY 2434 TTTGGAGTGTCCGGGAGCTGTACAGCACTACTACAGAGTCCGGTCCACCAATG 2493  
DB 241 TTTGGAGTGTCCGGGAGCTGTACAGCACTACTACAGAGTCCGGTCCACCAATG 300  
QY 2494 CTGCGCATTTGCTGATGCTCTCCAGAGAGCATGTATCAAGAAATTCACGACGAAAGC 2553  
DB 301 CTGCGCATTTGCTGATGCTCTCCAGAGAGCATGTATCAAGAAATTCACGACGAAAGC 360  
QY 2554 GACGCTTGAGAGCTGGGGGCTGTGTGTGGAGATTTTCACTTATGCAAAACGCTGG 2613  
DB 361 GACGCTTGAGAGCTGGGGGCTGTGTGTGGAGATTTTCACTTATGCAAAACGCTGG 420  
QY 2614 TACAGCTGTCAAACAATGAGTGTATGAGTATCACTCAGGGCCGAGTCTGCAAGCA 2673  
DB 421 TACAGCTGTCAAACAATGAGTGTATGAGTATCACTCAGGGCCGAGTCTGCAAGCA 480  
QY 2674 CCCCAGCATGCCCCCAGAGAGTGTATGAGTGTGGGGTCTGGCAGAGAGGCC 2733  
DB 481 CCCCAGCATGCCCCCAGAGAGTGTATGAGTGTGGGGTCTGGCAGAGAGGCC 540  
QY 2734 CACATGAGAGAAACATCAAGAGGATCCATACCTCTTCAGAACTTGGCCAGGCACT 2793  
DB 541 CACATGAGAGAAACATCAAGAGGATCCATACCTCTTCAGAACTTGGCCAGGCACT 600  
QY 2794 CCGGCTTACCTGAGCATTTCTAGGCTAG 2820  
DB 601 CCGGCTTACCTGAGCATTTCTAGGCTAG 627

RESULT 10  
LOCUS CB521879 846 bp mRNA linear EST 09-JUL-2003  
DEFINITION UI-M-GH0-ceo-k-15-0-UI.r1 NIH\_BMAP\_GH0 Mus musculus cDNA clone  
IMAGE:6842344 5', mRNA sequence.  
CB521879  
ACCESSION CB521879.1 GI:29355234  
VERSION EST.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 846)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: rgs@bgl-remail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/mousef.html  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.

FEATURES  
Location/Qualifiers

1..846  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6842344"  
/tissue\_type="whole brain"

/dev\_stage="1, 5, and 15 days newborn"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_id="NIH\_BMAP\_GH0"  
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;  
Site 2: Not I. The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to RNA size fraction, ligated  
with Ecor I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is CGAAGTGAAT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

## ORIGIN

Query Match 16.8%; Score 622.6; DB 6; Length 846;  
Best Local Similarity 85.5%; Pred. No. 2.6e-147;  
Matches 726; Conservative 0; Mismatches 118; Indels 5; Gaps 3;

QY 857 CAGACACTCAGAGATTTGACTGCTGATGAGAAACAGACAGAAATATTCCTGGCAACC 916  
DB 1 CCGACACTCAGAGATTTGACTGCTGATGAGAAACAGACAGAAATATTCCTGGCAACC 60  
QY 917 TGCAGATACCCATTTGTTGTTGTCATCTGCAAACTTGGCCGCACTTACCTGCTGG 976  
DB 61 TGCAGATACCCATTTGTTGTTGTCATCTGCAAACTTGGCCGCACTTACCTGCTGG 120  
QY 977 AGAAGAAAGTCTATACATATTCCTGATGTGGAGAGGATCCGGTCTCTAATAGT 1036  
DB 121 AGAAGAAAGTCTGATACCTTCTTCTGCAATGTGGGGGTGACCCACTCCCACTTGT 180  
QY 1037 ATTGGAGTGTGTGTAACCTGTTTCCAAACATATGAAAGCAAGCAGACAGAGGCT 1096  
DB 181 ACTGGAGCTTGGGAATTTGGTTTCCAAAGCAATGAAATGAAACAGACAGAGGCT 240  
QY 1097 CTTTAAAGATACCTAACATTTTCACTCCAGTGAAGAGTGGAGACAGATCTCTTGTGGCG 1156  
DB 241 CTTTAAAGATACCTAACATTTTCACTCCAGTGAAGAGTGGAGACAGATCTCTTGTGGCG 300  
QY 1157 AAAATCTTGAAGAAAGATGAATCTGTCAACCTCAGTGCATTTTGCACCACTA 1216  
DB 301 AAAATCTTGAAGAAAGATGAATCTGTCAACCTCAGTGCATTTTGCACCACTA 360  
QY 1217 TCACATTTTCTGATCTCCAACTCAGACCACTGGTGATTCATTCATCTGGAAG 1276  
DB 361 TCACATTTTCTGATCTCCAACTCAGACCACTGGTGATTCATTCATCTGGAAG 420  
QY 1277 GCAACCCCAACAGAGCTTCAAGTGTCTTATTAACGGGGCAATATTGAATGATCCAAAT 1336  
DB 421 GCAACCCCAACAGAGCTTCAAGTGTCTTATTAACGGGGCAATATTGAATGATCCAAAT 480  
QY 1337 ACATCTGTATCTAAATATCATCTTACCAATCAACAGAGATACCAAGGCTGCTCCAGCTGG 1396  
DB 481 ACATCTGTATCTAAATATCATCTTACCAATCAACAGAGATACCAAGGCTGCTCCAGCTGG 540  
QY 1397 ATAAATCCACTCAGATGAACAAATGGGGACTACCTTAAATGGCAAGAAATGATGGGA 1456  
DB 541 ATAAATCCACTCAGATGAACAAATGGGGACTACCTTAAATGGCAAGAAATGATGGGA 600  
QY 1457 AGATGAGAAACAGATTTCTGCTCACTTCATGGGCTGGATTCAGATGGTGCAT 1516  
DB 601 AGATGAGAAACAGATTTCTGCTCACTTCATGGGCTGGATTCAGATGGTGCAT - CGAGACA 659  
QY 1517 ACCCAATATTCCTGATGATATTTATGAAGTTATGGAATCGACGCAATGACATCGGG 1576  
DB 660 ACCCAATATTCCTGATGATATTTATGAAGTTATGGAATCGACGCAATGACATCGGG 716  
QY 1577 ACACCAAGAAAGAAATGAATATCCCTTCAAGAGCTCAGTGAATTAACCGGTCGGG 1636

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Db      717 ATATACGAACAAAGTAATGAATATCCCTCCACGAGATGTTGCTGACAAAGCAATGGG 776
Qy      1637 AACATCTCTGGTCTATGCTGTGGT-GATGATTCGCTCTGTGGGATTTTGGCTTTTG 1695
Db      777 AGCATCTCTGGTCTATGCGGTGGTGGTATTCGATCTGTGGGATTTCTGCTCTG 836
Qy      1696 GTAATGCTG 1704
Db      837 GTGATGTTG 845

RESULT 11
AL707530 615 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686f0348.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686f0348.5', mRNA sequence.
ACCESSION AL707530
VERSION AL707530.1 GI:19690885
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 615)
Lauber,J., Bahr,A., Mewes,H.W., Weill,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Lauber,J., Bahr,A., Mewes,H.W., Weill,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ) | Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686f0348) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..615
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686f0348"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: sf11A; Site_2: sf11B;
cDNA-collection"

ORIGIN
Query Match 16.5%; Score 611.8; DB 1; Length 615;
Best Local Similarity 99.7%; Pred. No. 1.4e-144;
Matches 613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1759 GTTATGACGATGATGATGATCTGCGACGCCCATGCAATCTCCAAATGGAGTAAC 1818
Db 1 GTTATGACGATGATGATGATGATCTGCGACGCCCATGCAATCTCCAAATGGAGTAAC 60

Qy 1819 ACTTCATCTTCTTGGAGAGTGCGCCAGATCTGTCATTTATGGAATGCCAAGATCCCT 1878
Db 61 ACTTCATCTTCTTGGAGAGTGCGCCAGATCTGTCATTTATGGAATGCCAAGATCCCT 120

Qy 1879 GTCAATGAAAATCCCGAGTACTTTGGCATCAACCAAGTCAGCTCAAGCCAGACATTT 1938
Db 121 GTCAATGAAAATCCCGAGTACTTTGGCATCAACCAAGTCAGCTCAAGCCAGACATTT 180

Qy 1939 GTTACGACATCAAGCCAGATTAATCTTTCTGAAAAGGAGCTAGGGAAGAGCCTTT 1998
Db 181 GTTACGACATCAAGCCAGATTAATCTTTCTGAAAAGGAGCTAGGGAAGAGCCTTT 240

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Qy 1999 GGAAGAGTGTCTAGCTGAATGCTATACCTCTGTCTGAGCAAGCAAGATCTTGGTG 2058
Db 241 GGAAGAGTGTCTAGCTGAATGCTATACCTCTGTCTGAGCAAGCAAGATCTTGGTG 300

Qy 2059 GCAATGAAAGCCCTGAAAGATGCGCAGTGAACAATGCAAGCAAGGACTTCCACCGTAAAGCC 2118
Db 301 GCAATGAAAGCCCTGAAAGATGCGCAGTGAACAAGCAAGGACTTCCACCGTAAAGCC 360

Qy 2119 GAGCTCTTGACCAACCTCCAGATGAGCAGATGCTCAAGTTCTATGAGCGTCTGCGTAG 2178
Db 361 GAGCTCTTGACCAACCTCCAGATGAGCAGATGCTCAAGTTCTATGAGCGTCTGCGTAG 420

Qy 2179 GCGGACCCCTCATCATGCTGTTTGAATGATGAATGAGATGAGGAACTTCAAGTTCTTC 2238
Db 421 GCGGACCCCTCATCATGCTGTTTGAATGATGAATGAGATGAGGAACTTCAAGTTCTTC 480

Qy 2239 AGGCGACAGCGCCCTGATGCGCGTGTGATGCGTGAAGGCAACCGCCCAAGGAATGACG 2298
Db 481 AGGCGACAGCGCCCTGATGCGCGTGTGATGCGTGAAGGCAACCGCCCAAGGAATGACG 540

Qy 2299 CAGTCGAGATGCTGATATATAGCCAGCAGATGCGCGGCGATGCTTACCTGCGCTCC 2358
Db 541 CAGTCGAGATGCTGATATATAGCCAGCAGATGCGCGGCGATGCTTACCTGCGCTCC 600

Qy 2359 CAGCACTTCTGTGAC 2373
Db 601 CAGCACTTCTGTGAC 615

RESULT 12
AL603196 601 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686j092.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686j092.5', mRNA sequence.
ACCESSION AL603196
VERSION AL603196.1 GI:1516702
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 601)
Wambut,R., Heubner,D., Mewes,H.W., Weill,B. and Wiemann,S.
EST (Wambut,R., Heubner,D., Mewes,H.W., Weill,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ) | Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686j092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..601
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/db_xref="taxon:9606"
/clone="DKFZp686j092"
/dev_stage="adult"
/lab_host="DH10B"
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cDNA-collection"

ORIGIN
Query Match 16.2%; Score 601; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 7.9e-142;

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Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 642 AATTGGATTCTGATTAATAATTTGGCTCAATAAGCATTTCTGAAAAAGCAACT 701
DB 1 AATTGGATTCTGATTAATAATTTGGCTCAATAAGCATTTCTGAAAAAGCAACT 60
QY 702 GCAGCATCATATTTTACCAGAAACAACTGACGAGTTTCTTGAGAAACATTTCCGTCA 761
DB 61 GCAGCATCATATTTTACCAGAAACAACTGACGAGTTTCTTGAGAAACATTTCCGTCA 120
QY 762 CCTTGACTTGTCTGAACTGATCCTGTGGGCAATCCATTTTCAATGCTCCGTGACATTA 821
DB 121 CCTTGACTTGTCTGAACTGATCCTGTGGGCAATCCATTTTCAATGCTCCGTGACATTA 180
QY 822 GTGATCAAGACTCTCCAGAGGCTAATCAAGTCCAGACACTGAGATTGTACTGCT 881
DB 181 GTGATCAAGACTCTCCAGAGGCTAATCAAGTCCAGACACTGAGATTGTACTGCT 240
QY 882 GAATGAAGAGCAAGAAATATTCCTGCGAAACCTGCAATGCCAATTGGTTGCC 941
DB 241 GAATGAAGAGCAAGAAATATTCCTGCGAAACCTGCAATGCCAATTGGTTGCC 300
QY 942 ATCTGCAATCTGGCCGACCTTAACCTCACTGTGAGAGAAAGAAAGTCTATCATTATC 1001
DB 301 ATCTGCAATCTGGCCGACCTTAACCTCACTGTGAGAGAAAGAAAGTCTATCATTATC 360
QY 1002 CTGTAGTGTGGAGGTATCCGTTCTTAATGATTTGGAGTGTGTAACCTGTTTC 1061
DB 361 CTGTAGTGTGGAGGTATCCGTTCTTAATGATTTGGAGTGTGTAACCTGTTTC 420
QY 1062 CAACATATGATGAATGAACCAAGCACAAGAGGCTCTTAAGATACTAATTTATC 1121
DB 421 CAACATATGATGAATGAACCAAGCACAAGAGGCTCTTAAGATACTAATTTATC 480
QY 1122 CGATGACAGTGGGAGAGAGATCTTGTGTGGCGGAAATCTTTAGAGAGATCAAGA 1181
DB 481 CGATGACAGTGGGAGAGAGATCTTGTGTGGCGGAAATCTTTAGAGAGATCAAGA 540
QY 1182 TTCTGTCAACTCACTGTGATTTTGAACCAATCTATCAATTTCCAAATCTCA 1241
DB 541 TTCTGTCAACTCACTGTGATTTTGAACCAATCTATCAATTTCCAAATCTCA 600
QY 1242 A 1242
DB 601 A 601

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RESULT 13
BP434087 893 bp mRNA linear EST 30-DEC-2003
LOCUS BP434087 full-length enriched swine cDNA library, adult lung Sus
DEFINITION BP434087 cDNA clone UNG010047802 5', mRNA sequence.
ACCESSION BP434087
VERSION BP434087.1 GI:40424154
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 893)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamashima,N. and Awata,T.
PEDS (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agricultural Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in

```

Animal Genome Research Program (Japan) by National Institute of Agricultural Sciences and STAFF-Institute Single pass sequencing of clones derived from oligo-capped cDNA library Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319 low quality bases were trimmed based on the quality values.

## FEATURES

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1..893
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/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="UNG010047802"
/tissue_type="lung"
/dev_stage="adult"
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lung"

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## ORIGIN

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Query Match 16.2%; Score 600.4; DB 5; Length 893;
Best Local Similarity 93.8%; Pred. No. 1.2e-141;
Matches 625; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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QY 1083 CCAACACAGGGCTCCTTAAGATTAATCAATTTCAATCCGATGACAGTGGAGCAGAT 1142
DB 1 CCAACACAGGGCTCCTTAAGATTAATCAATTTCAATCCGATGACAGTGGAGCAGAT 60
QY 1143 CTCTGTGTGGCGGAAATCTGTAGAGAGATCAAGATTTGTGCACTGCTGCA 1202
DB 61 CTCTGTGTGGCGGAAATCTGTAGAGAGATCAAGATTTGTGCACTGCTGCA 120
QY 1203 TTTTGGCAACAATCAATCAATTTCTGCAATCTCAACCTCAGACCACTGATGCTCC 1262
DB 121 TTTTGTCCAACTATCAATTTCTGCAATCTCAACCTCAGACCACTGATGCTCC 180
QY 1263 ATTCACTGTGAAGCAACCCCAACAGGCTTCACTGTTCTATTAAGGGGCAATTT 1322
DB 181 ATTCACTGTGAAGCAACCCCAACAGGCTTCACTGTTCTATTAAGGGGCAATTT 240
QY 1323 GAATGATCCAAATPACATCTGTACTAATAATCAATGTTACCAATCAACGAGTACCA 1382
DB 241 GAATGATCCAAATPACATCTGTACTAATAATCAATGTTACCAATCAACGAGTACCA 300
QY 1383 CTGCTTCACGCTGATTAATCTTCACTCATGAAACATGGGGAATCAAGTTAGTGGCAA 1442
DB 301 CTGCTTCACGCTGATTAATCTTCACTCATGAAACATGGGGAATCAAGTTAGTGGCAA 360
QY 1443 GAATGATGAGAGAGAGAGAGAAACAGATTTGTCTCACTTCATGAGGCTGGCTGGAAT 1502
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QY 1503 TGACGATGTGCAACCCCAATTAATCTGATGTAATTAAGATTAAGAACTGCAAC 1562
DB 421 TGACGATGTGCAACCCCAATTAATCTGATGTAATTAAGATTAAGAACTGCAAC 480
QY 1563 GAATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1622
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QY 1623 TAAACCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682
DB 541 TAAACCGGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 1683 ATTTGCTTTTGTGTAATGCTGTTTCTGCTTAAGTTGGCAAGACATTCAGATTGGCAT 1742
DB 601 ATTTGCTTTTGTGTAATGCTGTTTCTGCTTAAGTTGGCAAGACATTCAGATTGGCAT 660
QY 1743 GAAAGG 1748
DB 661 GAAAGG 666

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RESULT 14

BP250017  
 LOCUS BP250017 587 bp mRNA linear EST 15-SEP-2004  
 DEFINITION BP250017 Sugano cDNA library, hippocampus Homo sapiens cDNA clone  
 HPR01277, mRNA sequence.  
 ACCESSION BP250017  
 VERSION BP250017.1 GI:52132296  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 587)  
 Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,  
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 Genome Res. 14 (9), 1711-1718 (2004)  
 JOURNAL Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="HPR01277"  
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 Best Local Similarity 100.0%; Pred. No. 9.6e-138;  
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

461 AATGCAATGCTCTCCGATCTGTCGACGCCACCTTCTCCGCGATGTGGCAATTCGGA 520  
 Db 1 AATGCAATGCTCTCCGATCTGTCGACGCCACCTTCTCCGCGATGTGGCAATTCGGA 60  
 QY 521 GATTGAGCCTTAACAGTGTAGATCCTGAGAACATCACGAAATTTTCATGCAAAACGAGA 580  
 Db 61 GATTGAGCCTTAACAGTGTAGATCCTGAGAACATCACGAAATTTTCATGCAAAACGAGA 120  
 QY 581 AAAGGTTAGAAATCATCAACGAGAGATGTTGAGGTTATGTGGGACTGAGAAATCTGA 640  
 Db 121 AAAGGTTAGAAATCATCAACGAGAGATGTTGAGGTTATGTGGGACTGAGAAATCTGA 180  
 QY 641 CAATTGTGATCTGATTAATAATTTGTGCTCTAAAGCATTTCTGAAAAACGCAACC 700  
 Db 181 CAATTGTGATCTGATTAATAATTTGTGCTCTAAAGCATTTCTGAAAAACGCAACC 240  
 QY 701 TGACGACATCAATTTTAAACCGAACAACAGAGATTGTCTAGGAAACATTTCCGTC 760  
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 QY 821 TGTGATGCAAGACTCTCCAGAGGCTAAATCAGTCCAGACACTCAGAGATTGTGATGCC 880  
 Db 361 TGTGATGCAAGACTCTCCAGAGGCTAAATCAGTCCAGACACTCAGAGATTGTGATGCC 420  
 QY 881 TGAATGAAGCAGAGAAATTTCCCTGGCAACCTGAGAGATGCCAATGTGGTTGTC 940  
 Db 421 TGAATGAAGCAGAGAAATTTCCCTGGCAACCTGAGAGATGCCAATGTGGTTGTC 480  
 QY 941 CATCTGCAAAATCTGGCGCACTTAACCTCACTGTGAGAGAAAGTCTATCACTATAT 1000  
 Db 481 CATCTGCAAAATCTGGCGCACTTAACCTCACTGTGAGAGAAAGTCTATCACTATAT 540  
 QY 1001 CCGTAGTGTGGCAGGTGATCCGGTTCCTAATATGATATTGGGATG 1045

Db 541 CCGTAGTGTGGCAGGTGATCCGGTTCCTAATATGATATTGGGATG 585  
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 DEFINITION BP439194 full-length enriched swine cDNA library, adult lung sus  
 scrofa cDNA clone UMG010102603 5', mRNA sequence.  
 ACCESSION BP439194  
 VERSION BP439194.1 GI:40429261  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 REFERENCE 1 (bases 1 to 881)  
 Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,  
 Okumura,N., Hamasima,N. and Awata,T.  
 PDE (Pig EST Data Explorer): construction of a database for ESTs  
 derived from porcine full-length cDNA libraries  
 Nucleic Acids Res. 32 (1), D484-D488 (2004)  
 JOURNAL Contact: Hirohide Uenishi  
 Animal Genome Laboratory, Genome Research Department  
 National Institute of Agrobiological Sciences  
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
 Tel: +81-29-838-8627  
 Fax: +81-29-838-8627  
 Email: huenishi@affrc.go.jp  
 EST project with full-length enriched cDNA libraries carried out in  
 Animal Genome Research Program (Japan) by National Institute of  
 Agrobiological Sciences and STAFF-Institute  
 Single pass sequencing of clones derived from oligo-capped cDNA  
 library  
 Vector sequences were eliminated by RepeatMasker version 2002/07/13  
 and crossmatch version 0.990319  
 Low quality bases were trimmed based on the quality values.  
 Location/Qualifiers  
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 /clone="UMG010102603"  
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 /clone\_lib="full-length enriched swine cDNA library, adult  
 lung"

ORIGIN  
 Query Match 15.8%; Score 585; DB 5; Length 881;  
 Best Local Similarity 93.8%; Pred. No. 1.1e-137;  
 Matches 609; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

1100 TAAGATTAATCAATTTCCATCCGATGACAGTGGAGAGCAGATCTCTGTGTGGCGGAAA 1159  
 Db 2 TAAGATTAATCAATTTCCATCCGATGACAGTGGAGAGCAGATCTCTGTGTGGCGGAAA 61  
 QY 1160 ATCTTAGAGAGAGATCAAGATTCTGTCAACCTCACTGTGATTTGCAACCACTATCA 1219  
 Db 62 ATCTTAGAGAGAGATCAAGATTCTGTCAACCTCACTGTGATTTGCAACCACTATCA 121  
 QY 1220 CATTTCTGAAATCTCAACCTCAGACGACGACTGTGCATTTCCATTCATGTGAAAGCA 1279  
 Db 122 CATTTCTGAAATCTCAACCTCAGACGACGACTGTGCATTTCCATTCATGTGAAAGCA 181  
 QY 1280 ACCCCAAACGAGGCTTCAGTGGTTCTATTAACGGGGCAATTTGAATGAGTCCAAATACA 1339  
 Db 182 ACCCCAAACGAGGCTTCAGTGGTTCTATTAACGGGGCAATTTGAATGAGTCCAAATACA 241  
 QY 1340 TCTGTACTAAATATCATGTTATCAATCAACGAGATCAACGAGTGCCTCCAGCTGATA 1399  
 Db 242 TCTGTACTAAATATCATGTTATCAATCAACGAGATCAACGAGTGCCTCCAGCTGATA 301





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